



# SEQUENCE LISTING

<110> The Trustees of the University of Pennsylvania  
Wilson, James M.  
Gao, Guangping  
Alvira, Mauricio R.  
Vandenberghe, Luk H.

<120> Adeno-Associated Virus (AAV) Clades, Sequences, Vectors  
Containing Same, and Uses Therefor

<130> UPN-P3230PCT

<140> US 10/573,600  
<141> 2006-03-24

<150> US 60/508,226  
<151> 2003-09-30

<150> US 60/566,546  
<151> 2004-04-29

<160> 236

<170> PatentIn version 3.3

<210> 1  
<211> 2211  
<212> DNA  
<213> Unknown

<220>  
<223> adeno-associated virus, clone hu.31

<400> 1  
atggctgccc atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60  
gagtgggtggg ctttgaaacc tggagcccct caaccaagg caaatcaaca acatcaagac 120  
aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180  
aagggggagc cggtaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240  
cagcagctca aggccggaga caaccgtag ctcaagtaca accacgccga cgccgagttc 300  
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360  
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420  
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggatttggc 480  
aaatcgggtg cacagccgcg taaaagaga ctcaatttcg gtcagactgg cgacacagag 540  
tcagtcccg accctcaacc aatcggagaa cctcccgag cccctcagg tgtgggatct 600  
cttacaatgg cttcaggtgg tggcgacca gtggcagaca ataacgaagg tgccgatgga 660  
gtgggtagtt cctcgggaaa ttggcattgc gattccaat ggctggggga cagagtcac 720  
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatac 780  
tccaacagca catctggagg atcttcaaata gacaacgcct acttcggcta cagcaccccc 840  
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900  
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960  
cagggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020  
acggtccagg tcttcacgga ctgagactat cagctcccgt acgtgctcgg gtcggctcac 1080  
gagggctgcc tcccgcggt cccagcggac gttttcatga ttctcagta cgggtatctg 1140  
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct ttactgcct ggaatatctc 1200  
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260  
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320  
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380  
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggaccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa	1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct	1560
ggacctgcta tggccagcca caaagaagga gaggaccggt tctttccttt gtctggatct	1620
ttaatttttg gcaaacaaag aactggaaga gacaacgtgg atgcgagcaa agtcatgata	1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg	1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga	1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc	1860
aaaattcctc acacggacgg caactttcac ctttctccgc tgatgggagg gtttggaatg	1920
aagcaccgcg ctctctagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg	1980
gccttcaaca aggacaagct gaactctttc atcaccaggt attctactgg ccaagtcagc	2040
gtggagatcg agtgggagct gcagaagga aacagcaagc gctggaacct ggagatccag	2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaagggtga	2160
tatagtgaac cccgcccat tggcaccaga tacctgactc gtaatctgta a	2211

<210> 2  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.32

<400> 2	
atggctgccg atggttatct tccagattgg ctgcaggaca ctctctctga aggaataaga	60
cagtgggtga agtcaaaccc tggcccacca ccacaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccggcaa cggactcgac	180
aagggggagc cggtaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aggccggaga caaccgtac ctcaagtaca accacgccga cgccgagttc	300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct	420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggatttggc	480
aaatcgggtt cacagccgcg taaaaagaaa ctcaatttcg gtcagacttg cgacacagag	540
tcagtccccg accctcaacc aatcggagaa cctcccgag cccctcagg tgtgggatct	600
cttacaatgg cttcaggttg tggcgacca gtggcagaca ataacgaagg tgccgatgga	660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc	780
tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccctc	840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga	900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt	960
cagggtcaag aggttacgga caacaatgga gtcaagacca tcgccataaa ccttaccagc	1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac	1080
gagggctgcc tcccgcggt cccagcggac gttttcatga ttcctcagta cgggtatctg	1140
acgtttaatg atgggagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc	1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta	1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc	1320
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg	1380
ctaaaattca gcgtggccgg acccagcaac atggctgtcc aggggaagaaa ctacatacct	1440

ggaccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa	1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct	1560
ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct	1620
ttaatttttg gcaaacagg aactggaaga gacaacgtgg atgcggacaa agtcatgata	1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg	1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga	1800
atacttcctg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc	1860
aaaattcctc acacggacgg caactttcac ctttctccgc taatgggagg gtttggatg	1920
aagcaccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg	1980
gctttcaata aggacaagct gaactctttc atcaccaggt attctactgg ccaagtgcgc	2040
gtggagattg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag	2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaagggtga	2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a	2211

<210> 3  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus, human clone 9

<400> 3	
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc	60
gagtgggtggg ttttgaacc tggagccct caaccaagg caaatcaaca acatcaagac	120
aacgctcgag gtcttgtgct tccgggttac aaataccttg gaccggcaa cggactcgac	180
aagggggagc cggtaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aggcggaga caaccgtac ctcaagtaca accacgccga cgccgagttc	300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag	360
gccaaaaaga ggcttcttga acctcttggg ctggttgagg aagcggctaa gacggctcct	420
ggaaagaaga ggctgtaga gcagtctcct caggaaccgg actcctccgc gggatttggc	480
aatcgggtg cacagccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag	540
tcagtccag acctcaacc aatcggagaa cctcccgag cccctcagg tgtgggatct	600
cttacaatgg cttcaggtgg tggcgacca gtggcagaca ataacgaagg tgccgatgga	660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc	780
tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagaccccc	840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga	900
ctcatcaaca acaactggg attccggcct aagcgactca acttcaagct cttcaacatt	960
caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc	1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac	1080
gagggctgcc tcccgcggt cccagcggac gttttcatga ttcctcagta cgggtatctg	1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatctc	1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta	1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc	1320
gaccaatact tgtactatct ctcaaagact attaacgggt ctggacagaa tcaacaaacg	1380

ctaaaattca	gtgtggcccg	accagcaac	atggctgtcc	aggaagaaa	ctacatacct	1440
ggaccagct	accgacaaca	acgtgtctca	accactgtga	ctcaaaaca	caacagcgaa	1500
tttgcttggc	ctggagcttc	ttcttgggct	ctcaatggac	gtaatagctt	gatgaatcct	1560
ggacctgcta	tggccagcca	caaagaagga	gaggaccgtt	tctttccttt	gtctggatct	1620
ttaatttttg	gcaaacaagg	aactggaaga	gacaacgtgg	atgcggaaca	agtcatagata	1680
accaacgaag	aagaaattaa	aactactaac	ccggtagcaa	cggagtccta	tggacaagtg	1740
gccacaaacc	accagagtgc	ccaagcacag	gcgcagaccg	gctgggttca	aaaccaagga	1800
atacttccgg	gtatgggttg	gcaggacaga	gatgtgtacc	tgcaaggacc	catttggggc	1860
aaaattcctc	acacggacgg	caactttcac	ccttctccgc	tgatgggagg	gtttggaatg	1920
aagcaccgcg	ctcctcagat	cctcatcaaa	aacacacctg	tacctgcgga	tcctccaacg	1980
gccttcaaca	aggacaagct	gaactctttc	atcaccagct	atttacttgg	ccaagtcagc	2040
gtggagatcg	agtgggagct	gcagaaggaa	aacagcaagc	gctggaaccc	ggagatccag	2100
tacacttcca	actattacaa	gtctaataat	gttgaatttg	ctgttaatac	tgaagggtga	2160
tatagtgaac	cccgcccat	tggcaccaga	tacctgactc	gtaatctgta	a	2211

<210> 4  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.17

<400>	4					
atggctgccg	atggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtgggtgg	acttgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctgc	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgaca	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggagcgc	agtcttcag	360
gccaagaagc	gggttctcga	acctctcggt	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccatcaccc	cagcgttctc	cagactcctc	tacgggcatc	480
ggcaagacag	gccagcagcc	gcgaaaaag	agactcaact	ttgggcagac	tggcgactca	540
gagtcagtgc	ccgaccctca	accaatcgga	gaaccccccg	caggccctc	tggcttgagg	600
tctggtacaa	tggctgcagg	cggtggcgct	ccaatggcag	acaataacga	aggcgccgac	660
ggagtgggta	gttcttcagg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggccctc	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacatcggg	aggaagcacc	aacgacaaca	cctacttcgg	ctacagcacc	840
ccctgggggt	atcttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcaacttcaa	gctcttcaac	960
atccaggtca	aggaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taaccttacc	1020
agcacgattc	aggtctttac	ggactcgga	taccagctcc	cgtacgtcct	cggctctgcg	1080
caccagggct	gcccgcctcc	gttcccggcg	gacgtcttca	tgattctcta	gtacgggtac	1140
ctgactctga	acaacggcag	tcaggccgtg	ggccgttcct	ccttctactg	cctggagtac	1200
tttcttctc	aatgcggag	aacgggcaac	aactttgagt	tcagctacca	gtttgaggac	1260
gtgccttttc	acagcagcta	gcgcatagc	caaagcctgg	accggctgat	gaacccccctc	1320
atcgaccagt	acctgtacta	cctgtctcgg	actcagtcca	cgggaggtac	cgcagggaact	1380

cagcagttgc	tatttttctca	ggccgggcct	aataacatgt	cggctcaggc	caaaaactgg	1440
ctaccggg	cctgctaccg	gcagcaacgc	gtctccacga	cactgtcgca	aaataacaac	1500
agcaactttg	cttggaccgg	tgccaccaag	tatcatctga	atggcagaga	ctctctggta	1560
aatcccgggtg	tcgctatggc	aacgcacaag	gacgacgaag	agcgattttt	tccatccagc	1620
ggagtcttga	tgtttgggaa	acagggagct	ggaaaagaca	acgtggacta	tagcagcggt	1680
atgctaacca	gtgaggaaga	aatcaaaacc	accaaccag	tggccacaga	acagtacggc	1740
gtggtggccg	ataacctgca	acagcaaac	gccgctccta	ttgtaggggc	cgtaacagt	1800
caaggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtaacctga	gggtcctatc	1860
tgggccaaga	ttcctcacac	ggacggcaac	tttcatcctt	cgccgctgat	gggaggcttt	1920
ggactgaaac	acccgcctcc	tcagatcctg	attaagaata	cacctgttcc	cgcggtacct	1980
ccaactacct	tcagtcaagc	caagctggcg	tcgttcatca	cgcagtacag	caccggacag	2040
gtcagcgtag	aaattgaaatg	ggagctgcag	aaagagaaca	gcaagcgctg	gaaccagag	2100
attcagtata	cttccaacta	taacaaatct	gttaatgtgg	actttactgt	ggacactaat	2160
ggtgtgtatt	cagagcctcg	ccccattggc	accagatacc	tgactcgtaa	tctgtaa	2217

<210> 5  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.6

<400>	5	
atggctgccc	atggttatct	tccagattgg
gagtgggtggg	acttgaaacc	tggagccccg
gacggccggg	gtctggtgct	tcctggctac
aaggggggagc	ccgtcaacgc	ggcggacgca
cagcagctca	aagcgggtga	caatccgtac
caggagcgtc	tgcaagaaga	tacgtctttt
gccaagaagc	gggttctcga	acctctcggg
ggaaagaaga	gaccggtaga	gccatcaccc
ggcaagacag	gccagcagcc	cgcaaaaag
gagtcagtg	ccgacctca	accaatcgga
tctggtacaa	tggctgcagg	cggtggcgct
ggagtgggta	gttcctcagg	aaattggcat
atcaccacca	gcaccgacc	ctgggccctc
atctccaacg	ggacatcggg	aggaagcacc
ccctgggggt	attttgactt	taacagattc
cgactcatca	acaacaactg	gggattccgg
atccaggtca	aggaggtcac	gcagaatgaa
agcacgattc	aggtctttac	ggactcggaa
caccagggct	gcccgcctcc	gttcccggcg
ctgactctga	acaacggcag	tcaggccgtg
tttctttctc	aaatgcggag	aacgggcaac
gtgccttttc	acagcagcta	cgcgcatagc

atcgaccagt	acctgtacta	cctgtctcgg	actcagtcca	cgggaggtac	cgcaggaact	1380
cagcagttgc	tattttctca	ggccgggcct	aataacatgt	cggctcaggc	caaaaactgg	1440
ctaccggg	cctgtaccg	gcagcaacgc	gtctccacga	cactgtcgca	aaataacaac	1500
agcaactttg	cttggaccgg	tgccaccaag	tatcatctga	atggcagaga	ctctctggta	1560
aatcccgggt	tcgctatggc	aacgcacaag	gacgacgaag	agcgattttt	tccatccagc	1620
ggagtcttga	tgtttgggaa	acagggagct	ggaaaagaca	acgtggacta	tagcagcggt	1680
atgctaacca	gtgaggaaga	aatcaaaacc	accaaccag	tggccacaga	acagtacggc	1740
gtggtggccg	ataacctgca	acagcaaaac	gccgctccta	ttgtaggggc	cgtcaacagt	1800
caaggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatc	1860
tgggccaaga	ttcctcacac	ggacggcaac	tttcatcctt	cgccgctgat	gggaggcttt	1920
ggactgaaac	acccgcctcc	tcagatcctg	attaagaata	cacctgttcc	cgcggtacct	1980
ccaactacct	tcagtcaagc	caagctggcg	tcgttcatca	cgcagtacag	caccggacag	2040
gtcagcgtag	aaattgaatg	ggagctgcag	aaagagaaca	gcaagcgctg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgctgt	caatactgag	2160
ggtaattatt	cagagcctcg	ccccattggc	accggttacc	tcaccgtaaa	cctgtaa	2217

<210> 6  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.41

<400>	6	
atggctgctg	acggttatct	tccagattgg
gagtgggtgg	acctgaaacc	tggagcccc
gacggccggg	gtctggtgct	tcctggctac
aagggggagc	ccgtcaacgc	ggcggacgca
cagcagctca	aagcgggtga	caatccgtac
caggagcgtc	tacaagaaga	tacgtctttt
gccaagaagc	gggttctcga	acctctcggg
ggaaagaaga	gaccggtaga	accgccacct
ggcaagaaag	gccagcagcc	cgctaaaaag
gagtcagtcc	ccgacctca	accaatcgga
tctggtacaa	tggctgcagg	cggtggcgct
ggagtgggta	gttcctcagg	aaattggcat
atcaccacca	gcaccgaac	ctgggccctg
atatccaatg	ggacatcggg	aggaagcacc
ccctgggggt	attttgactt	caacagattc
cgactcatca	acaacaactg	gggattccgg
atccagggtca	aggagggtcac	gcagaatgaa
agcacgattc	aggtattttac	ggactcggaa
caccagggct	gcctgcctcc	gttcccggcg
cttacctga	acaatggaag	tcaagccgta
tttccatctc	aaatgctg	aactggaaac
gtgcctttcc	acagcagcta	cgcacacagc

atcgaccagt	acctgtacta	cttatccaga	actcagtcca	caggaggaac	tcaaggtacc	1380
cagcaattgt	tattttctca	agctgggctt	gcaaacaatgt	cggctcaggc	taagaactgg	1440
ctacctggac	cttgctaccg	gcagcagcga	gtctctacga	cactgtcgcga	aaacaacaac	1500
agcaactttg	cttggtactg	tgccaccaa	tatcacctga	acggaagaga	ctctttggta	1560
aatcccgggtg	tcgccatggc	aaccacaag	gacgacgagg	aacgcttctt	cccgtcgagt	1620
ggagtccctga	tgtttgga	acaggtgct	ggaagagaca	atgtggacta	cagcagcggt	1680
atgctaacca	gcgaagaaga	aattaaaacc	actaacctg	tagccacaga	acaatacgg	1740
gtggtggctg	acaacttgca	gcaaaccaat	acagggccta	ttgtgggaaa	tgtcaacagc	1800
caaggagcct	tacctggcat	ggtctggcag	aaccgagacg	tgtacctgca	gggtcccatc	1860
tgggccaaga	ttcctcacac	ggacggcaac	ttccaccctt	caccgcta	gggaggattt	1920
ggactgaagc	accacctcc	tcagatcctg	atcaagaaca	cgccggtacc	tgcggtacct	1980
ccaacaacgt	tcagccaggc	gaaattggct	tccttcatta	cgcagtacag	caccggacag	2040
gtcagcgtg	aaatcgagt	ggagctgcag	aaggagaaca	gcaaacgtg	gaaccagag	2100
attcagtaca	cttcaacta	ctacaaatct	acaaatgtg	actttgctgt	caatacagag	2160
ggaacttatt	ctgagcctcg	ccccattggt	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 7  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.38

<400>	7					
atggctgctg	acggttatct	tccagattgg	ctcaggagaca	acctctctga	gggcattcgc	60
gagtggtggg	acctgaaacc	tggagcccc	aagccaagg	ccaaccagca	gaagcaggac	120
gacggccggg	gtctggtgct	tcctggttac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgccgagttt	300
caggagcgtc	tacaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggt	ctggttgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaag	gccagcggcc	cgctaaaaag	agactgaact	ttggtcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	accaatcgga	gaaccaccag	caggccccctc	tggtctggga	600
tctgtgtaca	tggtctcagg	cgggtggcgt	ccaatggcag	acaataacga	aggcgcggac	660
ggagtgggta	gttcctcagg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcacccgaac	ctgggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atatccaatg	ggacatcggg	aggaagcacc	aacgacaaca	cctacttcgg	ctacagcacc	840
ccctgggggt	atthtgactt	caacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	ccaaaaagac	tcagcttcaa	gcccttcaac	960
atccaggtca	aggaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taaccttacc	1020
agcacgattc	aggtattttac	ggactcggaa	taccagctgc	cgtacgtcct	cggctccgcg	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcccca	gtacggctac	1140
cttactactga	acaatggaag	tcaagccgta	ggccgttcct	ccttctactg	cctggaatat	1200
tttccatctc	aaatgctgcg	aactggaaac	aattttgaat	tcagctacac	cttcgaggac	1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc	1320
atcgaccagt acctgcaacta cttatccaga actcagtcca caggaggaac tcaagggtacc	1380
cagcaattgt tatttttctca agctgggcct gcaaacaatgt cggctcaggc taagaactgg	1440
ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac	1500
agcaactttg cttggactgg tgccacaaa tatcacctga acggaagaga ctctttggta	1560
aatcccgggtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcgagt	1620
ggagtcctga tgtttgaaa acaggggtgt ggaagagaca atgtggacta cagcagcgtt	1680
atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggg	1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc	1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggctccatc	1860
tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaata gggaggattt	1920
ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccgggtacc tgcggatcct	1980
ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag	2040
gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaaccagag	2100
attcagtaca cttcaacta ctacaaatct acaaatgtgg actttgtgt caatacagag	2160
ggaacttatt ctgagcctcg ccccatgtgt actcgctacc tcaccgtaa tctgtaa	2217

<210> 8  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.42

<400> 8	
atggctgctg acggttatct tccagattgg ctgaggagaca acctctctga gggcattcgc	60
gagtggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aaggggggagc ccgtcaacgc ggcgagcga gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagcggctaa gacggctcct	420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaagc gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccctc tggctcggga	600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac	660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa	780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc	840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac	960
atccagggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc	1020
agcacgattc aggtatttac ggactcgga taccagctgc cgtacgtcct cggctccgcg	1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattccca gtacggctac	1140
cttacctga acaatggaag tcaagccgta ggccgttcct ctttctactg cctggaatat	1200
tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac	1260

gtgcctttcc	acagcagcta	cgcacacagc	cagagcttgg	accgactgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cttatccaga	actcagtcca	caggaggaaac	tcaagggtacc	1380
cagcaattgt	tattttctca	agctgggcct	gcaaacatgt	cggtcagggc	taagaactgg	1440
ctacctggac	cttgctaccg	gcagcagcga	gtctctacga	cactgtcgca	aagcaacaac	1500
agcaactttg	cttgacttgg	tgccaccaa	tatcacctga	acggaagaga	ctctttggta	1560
aatcccgggt	tcgccatggc	aaccacaag	gacgacgagg	aacgcttctt	cccgtcgagt	1620
ggagtctga	tggttgaaa	acagggtgct	ggaagagaca	atgtggacta	cagcagcggt	1680
atgctaacca	gcgaagaaga	aattaaaacc	actaacctg	tagccacaga	acaatacggt	1740
gtggtggctg	acaacttgca	gcaaaccaat	acagggccta	ttgtgggaaa	tgtcaacagc	1800
caaggagcct	tacctggcat	ggtctggcag	aaccgagacg	tgtacctgca	gggtcccatc	1860
tgggccaaga	ttcctcacac	ggacggcaac	ttccaccctt	caccgcta	atggaggactt	1920
ggactgaagc	accacctcc	tcagatcctg	atcaagaaca	cgccgggtacc	tgcggtatcct	1980
ccaacaacgt	tcagccaggc	gaaattggct	tccttcatta	cgcagtacag	caccggacag	2040
gtcagcgtgg	aaatcgagtg	ggagctgcag	aaggagaaca	gcaaacgctg	gaaccagag	2100
attcagtaca	cttcaacta	ctacaaatct	acaaatgtgg	actttgtgtg	caatacagag	2160
ggaacttatt	ctgagcctcg	ccccattggt	actcgttacc	tcaccgtaa	tctgttaa	2217

<210> 9  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.72

<400>	9					
atggctgctg	acggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtggtggg	acctgaaacc	tggagcccc	aagcccaagg	ccaaccagca	gaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggagcag	agtcttcag	360
gccaagaagc	gggttctcga	acctctcggt	ctggttgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaag	gccagcagcc	cgtaaaaag	agactgaact	ttggtcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	accaatcgga	gaaccaccag	caggccctc	tggtctggga	600
tctggtacaa	tggtcgagg	cggtggcgct	ccaatggcag	acaataacga	aggcgcgac	660
ggagtgggta	gttcttcagg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggccctg	cccactaca	acaaccacct	ctacaagcaa	780
atatccaatg	ggacatcggg	aggaagcacc	aacgacaaca	cctacttcgg	ctacagcacc	840
ccctgggggt	attttgactt	caacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	ccaaaagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aggaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taaccttacc	1020
agcacgattc	aggtattttac	ggactcgga	taccagctgc	cgtacgtcct	cggctccgcg	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcccca	gtacggctac	1140
cttacctga	acaatggaag	tcaagccgta	ggccgttcct	ccttctactg	cctggaatat	1200

tttccatctc	aaatgctg	aactggaaac	aatTTTgaat	tcagctacac	cttcgaggac	1260
gtgcctttcc	acagcagcta	cgcacacagc	cagagcttgg	accgactgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cttatccaga	actcagtgcca	caggaggaac	tcaagggtacc	1380
cagcaattgt	tattttctca	agctgggcct	gcaaacaatgt	cggctcaggc	taagaactgg	1440
ctacctggac	cttgctaccg	gcagcagcga	gtctctacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cttggtactgg	tgccaccaa	tatcacctga	acggaagaga	ctctttggta	1560
aatcccgggtg	tcgcatggc	aaccacaag	gacgacgagg	aacgcttctt	cccgtcgagt	1620
ggagtcctga	tgtttgaaa	acaggtgct	ggaagagaca	atgtggacta	cagcagcggt	1680
atgctaacca	gcgaagaaga	aattaaaacc	actaacctg	tagccacaga	acaatacgggt	1740
gtggtggctg	acaacttgca	gcaaaccaat	acagggccta	ttgtgggaaa	tgtcaacagc	1800
caaggagcct	tacctggcat	ggtctggcag	aaccgagacg	tgtacctgca	gggtcccatc	1860
tgggccaaga	ttctcacac	ggacggcaac	ttccaccctt	caccgcta	gggaggattt	1920
ggactgaagc	acccacctcc	tcagatcctg	atcaagaaca	cgccggtacc	tgcggatcct	1980
ccaacaacgt	tcagccaggc	gaaattggct	tccttcatta	cgcagtacag	caccggacag	2040
gtcagcggtg	aaatcgagt	ggagctgcag	aaggagaaca	gcaaacgctg	gaaccagag	2100
attcagtaca	cttcaacta	ctacaatct	acaaatgtg	actttgctgt	caatacagag	2160
ggaacttatt	ctgagcctcg	ccccattggt	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 10  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.37

<400> 10	
atggctgctg	acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtgg	acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg	gtctgggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc	ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca	aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc	tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagaagc	gggttctcga acctctcgggt ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga	gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac 480
ggcaagaaag	gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtc	ccgaccctca accaatcgga gaaccaccag caggccctc tggctctggga 600
tctggtacaa	tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
ggagtgggta	gttcctcagg aaattggcat tgcgattcca catggctggg cgaacagagtc 720
atcaccacca	gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
atatccaatg	ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt	attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca	acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
atccagggtca	aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
agcacgattc	aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080
caccagggct	gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
cttacctga	acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc	aaatgctg	cg aactggaaac	aattttgaat	tcagctacac	cttcgaggac	1260
gtgcctttcc	acagcagcta	cgacacacagc	cagagcttgg	accgactgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cttatccaga	actcagtcca	caggaggaac	tcaaggtacc	1380
cagcaattgt	tattttctca	agctgggcct	gcaaacatgt	cggtcaggc	taagaactgg	1440
ctacctggac	cttgctaccg	gcagcagcga	gtctctacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cttggtactg	tgccaccaa	tatcacctga	acggaagaga	ctctttggta	1560
aatcccgggtg	tcgccatggc	aaccacaag	gacgacgagg	aacgcttctt	cccgtcgagt	1620
ggagtcctga	tggtcggaaa	acaggtgct	ggaagagaca	atgtggacta	cagcagcggt	1680
atgctaacca	gcgaagaaga	aattaaaacc	actaaccctg	tagccacaga	acaatacggg	1740
gtggtggctg	acaacttgca	gcaaaccaat	acagggccta	ttgtgggaaa	tgtcaacagc	1800
caaggagcct	tacctggcat	ggctctggcag	aaccgagacg	tgtacctgca	gggtcccatc	1860
tgggccaaga	ttcctcacac	ggacggcaac	ttccaccctt	caccgcta	at gggaggattt	1920
ggactgaagc	accacctcc	tcagatcctg	atcaagaaca	cgccggtacc	tgcggtatcct	1980
ccaacaacgt	tcagccaggc	gaaattggct	tccttcatta	cgagtagacag	caccggacag	2040
gtcagcgctg	aaatcgagtg	ggagctgcag	aaggagaaca	gcaaacgctg	gaaccagag	2100
attcagtaca	cttcaacta	ctacaaatct	acaaatgtgg	actttgctgt	caatacagag	2160
ggaacttatt	ctgagcctcg	ccccattggt	actcggtacc	tcaccgtaa	tctgtaa	2217

<210> 11  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.40

<400> 11	
atggctgctg	acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtggtggg	acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg	gtctggtgct tcctggctac aagtacctcg gaccctcaa cggactcgac 180
aagggggagc	ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca	aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgct	tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc	gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga	gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac 480
ggcaagaag	gccagcagcc cgctaaaaag agactgagct ttggtcagac tggcgactca 540
gagtcagtcc	ccgaccctca accaatcgga gaaccaccag caggccctc tggctcggga 600
tctggtacaa	tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
ggagtgggta	gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca	gcaccgaac ctgggcctg cccacctaca acaaccacct ctacaagcaa 780
atatccaatg	ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt	attttgactt caacagattc cactgccact tctaccacg tgactggcag 900
cgactcatca	acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
atccagggtca	aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
agcacgattc	aggtattttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080
caccagggct	gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ctttctactg cctggaatat	1200
tttccatctc aaatgctgcg aactggaaac aattctgaat tcagctacac cttcgaggac	1260
gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc	1320
atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc	1380
cagcaattgt tattttctca agctgggcct gcaaacaatgt cggctcaggc taagaactgg	1440
ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac	1500
agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta	1560
aatcccgggt tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcgagt	1620
ggagtccctga tgtttgaaa acaggggtgt ggaagagaca atgtggacta cagcagcgtt	1680
atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacgg	1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc	1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggccccatc	1860
tgggccaaga ttctctacac ggacggcaac ttccaccctt caccgctaata gggaggattt	1920
ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccgggtacc tgcggatcct	1980
ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag	2040
gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaaccagag	2100
attcagtaca cttcaacta ctacaaatct acaaatgtgg actttgtgt caatacagag	2160
ggaacttatt ctgagcctcg cccattgggt actcgttacc tcaccgtaa tctgtaa	2217

<210> 12  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.38

<400> 12	
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtgggtgg acctgaaacc tggagcccc aagccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcgagcga gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag	360
gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct	420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaaag gccagcagcc cgtaaaaag agactgaact ttggtcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccacctg caggccctc tggctctggga	600
tctgtgataa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac	660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa	780
atatccaatg ggacatcggg agggagcacc aacgacaaca cctacttcgg ctacagcacc	840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac	960
atccagggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc	1020
agcacgattc aggtatttac ggactcgga taccagctgc cgtacgtcct cggctccgcg	1080
caccagggtc gcctgcctcc gttccggcg gacgtcttca tgattccca gtacggctac	1140

cttacctga	acaatggaag	tcaagccgta	ggccgttcct	ccttctactg	cctggaatat	1200
tttccatctc	aatgctgcg	aactggaaac	aattttgaat	tcagctacac	cttcgaggac	1260
gtgcctttcc	acagcagcta	cgcacacagc	cagagcttgg	accgactgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cttatccaga	actcagtcca	caggaggaaac	tcaagggtacc	1380
cagcaattgt	tattttctca	agctgggcct	gcaaacaatgt	cggctcaggc	taagaactgg	1440
ctacctggac	cttgctaccg	gcagcagcga	gtctctacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cttggtactg	tgccacaaa	tatcacctga	acggaagaga	ctctttggta	1560
aatcccggtg	tcgccatggc	aaccacaag	gacgacgagg	aacgtttctt	cccgtcgagt	1620
ggagtccctga	tgtttgaaa	acaggggtgt	ggaagagaca	atgtggacta	cagcagcggt	1680
atgctaacca	gcgaagaaga	aattaaaacc	actaacctg	tagccacaga	acaatacggg	1740
gtggtggctg	acaacttgca	gcaaaccaat	acagggccta	ttgtgggaaa	tgtcaacagc	1800
caaggagcct	tacctggcat	ggtctggcag	aaccgagacg	tgtacctgca	gggtcccatc	1860
tgggccaaga	ttctcacac	ggacggcaac	tgccaccctt	caccgcta	gggaggattt	1920
ggactgaagc	acccacctcc	tcagatcctg	atcaagaaca	cgccgggtacc	tgccggatcct	1980
ccaacaacgt	tcagccaggc	gaaattggct	tccttcatta	cgcagtacag	caccggacag	2040
gtcagcgctg	aaatcgagt	ggagctgcag	aaggagaaca	gcaaacgctg	gaaccagag	2100
attcagtaca	cttcaacta	ctacaaatct	acaaatgtgg	actttgctgt	caatacagag	2160
ggaacttatt	ctgagcctcg	ccccattggt	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 13  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.39

<400>	13					
atggctgctg	acggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtggtggg	acctgaaacc	tggagcccc	aagcccaagg	ccaaccagca	gaagcaggac	120
gacggccggg	gtctgggtgct	tcctggctac	aagtacctcg	gaccttca	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaaag	gccagcagcc	cgctaaaaag	agactgaact	ttggtcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	accaatcgga	gaaccaccag	caggccctc	tggctggga	600
tctggtacaa	tggtgcagg	cggtggcgct	ccaatggcag	acaataacga	aggcgccgac	660
ggagtgggta	gttctctcagg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctggggcctg	cccacctaca	acaaccacct	ctacaagcaa	780
atatccaatg	ggacatcggg	aggaagcacc	aacgacaaca	cctacttcgg	ctacagcacc	840
ccctgggggt	atcttgactt	caacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	ccaaaaagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aggaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taaccttacc	1020
agcacgattc	aggtattttac	ggactcggaa	taccagctgc	cgtacgtcct	cggctccgcg	1080

caccagggct gcctgcctcc gttccccggcg gacgtcttca tgattcccca gtacggctac	1140
cttacactga acaatggaag tcaagccgta ggccgttcct ctttctactg cctggaatat	1200
tttccatctc aaatgctgcy aactggaaac aattttgaat tcagctacac cttcaggagac	1260
gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc	1320
atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaaac tcaagggtacc	1380
cagcaattgt tattttctca agctgggcct gcaaaccatgt cggctcaggc taagaactgg	1440
ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac	1500
agcaactttg cttggactgg tgccaccaa tatcacctga acggaagaga ctctttggta	1560
aatcccgggt tgcgccatgg aaccacaag gacgacgagg aacgcttctt cccgtcgagt	1620
ggagtcttga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt	1680
atgctaacca gcgaagaaga aattaaacc actaacctg tagccaaga acaatacgg	1740
gtggtggctg ataacttgca gcaaaccaat acggggccta ttgtgggaaa tgtcaacagc	1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggccccatc	1860
tgggccaaaga ttctctcacac ggacggcaac ttccaccctt caccgcta at gggaggattt	1920
ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccgggtacc tgcggatcct	1980
ccaacaacgt tcagccaggc gaaattggct tccttcatta cgagtacag caccggacag	2040
gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaaccagag	2100
attcagtaca cttcaaaact ctacaaatct acaaatgtgg actttgctgt caatacagag	2160
ggaacttatt ctgagcctcg ccccatgtgt actcgttacc tcaccgtaa tctgtaa	2217

<210> 14  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.40

<400> 14	
atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc	60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctg gaccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctg agcacgaca ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct	420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac	480
ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccctc tggctctggga	600
tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac	660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa	780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc	840
ccctgggggt attttgactt caacagattc cactgccact tctcaccag tgactggcag	900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac	960
atccaggctca aggaggtcac gcaggatgaa ggcaccaaga ccacgcgcaa taaccttacc	1020
agcacgattc aggtatttac ggactcgga taccagctgc cgtacgtcct cggctccgcg	1080

caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcccca	gtacggctac	1140
cttacctga	acaatggaag	tcaagccgta	ggccgttcct	ccttctactg	cctggaatat	1200
tttccatctc	aaatgtcgcg	aactggaaac	aattttgaat	tcagctacac	cttcgaggac	1260
gtgcctttcc	acagcagcta	cgcacacagc	cagagcttgg	accgactgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cttatccaga	actcagtcca	caggaggaac	tcaaggtacc	1380
cagcaattgt	tattttctca	agctgggcct	gcaaacatgt	cggctcgggc	taagaactgg	1440
ctacctggac	cttgctaccg	gcagcagcga	gtctctacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cttggtactg	tgccaccaaa	tatcacctga	acggaagaga	ctctttggta	1560
aatcccgggt	ttgctatggc	aacgcataag	gacgacgagg	aacgtttctt	tccatcgagc	1620
ggagtcctga	tgtttggaag	acaggggtgt	ggaagagaca	atgtggacta	tagcagcggt	1680
atgctaacca	gcgaggaaga	aattaaaacc	actaaccttg	tagccacaga	acaatacggg	1740
gtggtggctg	acaacttgca	gcaagccaat	acagggccta	ttgtgggaaa	tgtcaacagc	1800
caaggagcct	tacctggcat	ggctctggcag	aaccgagacg	tgtacctgca	gggtcccatc	1860
tggggcaaaa	ttcctcacac	ggacggcaat	tttcaccctg	ctcctctgat	gggctggctt	1920
ggactgaagc	accacctccc	ccagatcctg	atcaagaata	cgccgggtacc	tgcggtatcct	1980
ccaacgacgt	tcagccaggc	aaaattgggt	tccttcatca	cgcagtacag	caccggccag	2040
gtcagcgtgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgatg	gaaccagaa	2100
attcagtaca	cttccaacta	ctacaaatct	acaaatgtgg	actttgtgtg	caattctgag	2160
ggtacatatt	cagagcctcg	ccccattggg	actcgttatc	tgacacgtaa	tctgtaa	2217

<210> 15  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.64

<400> 15	
atggctgccc	atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtggtggg	acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg	gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aaggggggagc	ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca	aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caggagcgtc	tgcaagaaga tacgtctttt gggggcaacc tcgggagcagc agtcttccag 360
gccaagaagc	gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga	gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaag	gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
gagtcagtcc	ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600
tctggtacaa	tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac 660
ggagtgggta	gttctctggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca	gcaccgaac ctgggcccctg ccacactaca acaaccacct ctacaagcaa 780
atctccaacg	ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840
ccctgggggt	attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca	acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
atccagggtca	aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc	1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac	1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct ctttctactg cctggagtac	1200
ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcaggagac	1260
gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc	1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc	1380
cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg	1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg	1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc	1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt	1860
tgggccaaga ttctctcacac agatggcaac ttccaccgt ctcctttaat gggcggcttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagtgaat tctttcatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgtgtg ggagctgcag aaggagaaca gcaagcgcag gaaccagag	2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgtgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatggc actcgttacc tcaccgtaa tctgtaa	2217

<210> 16  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.68

<400> 16	
atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtgggtgg acctgaaacc tggagccccg aaaccctaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcagacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaagc gccagcagcc cgcgagaag agactcaatt tcggtcagac tggcgactca	540
gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga	600
tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac	660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctggggcctg cccacctaca acaaccacct ctacaagcaa	780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960
atccagggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc	1020

agcaccatcc	aggtgtttac	ggactcggaa	taccagctgc	cgtacgtcct	cggctctgcc	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttcccctctc	agatgctgag	aacgggcaac	aacttttcct	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	accagttcta	cgggaggcac	agcgggaacc	1380
cagcagttgc	tgttttctca	ggccgggcct	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccgggcg	tcgccatggc	aaccaacaag	gacgacgagg	accgcttctt	cccaccagc	1620
ggcatcctca	tgtttggaac	gcaggggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaac	accgctccta	ttgtgggggc	cgtcaacagc	1800
caggggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttcctcacac	agatggcaac	tttcacccgt	ctcctttaat	ggcggtcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaca	ctcctgttcc	tgcggtcctt	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatca	cgcagtacag	caccggacaa	2040
gtcagcgtgg	tgatcgagtg	ggagctgcag	aaggagaaca	gcaagcgtg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgctgt	taatactgag	2160
ggtgtttact	ctgagcttcg	ccccattggc	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 17  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.53

<400> 17	
atggctgccc	atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg	acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg	gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc	ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca	aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caggagcgtc	tgcaagaaga tacgtctttt gggggcaacc tcgggagcagc agtcttccag 360
gccaagaagc	gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga	gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag	gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
gagtcagtcc	ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600
tctggtacaa	tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660
ggagtgggta	gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca	gcacccgaac ctggggccctg cccacctaca acaaccacct ctacaagcaa 780
atctccaacg	ggacctcggg aggcagcacc aacgacaaca cctacttttg ctacagcacc 840
ccctgggggt	attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca	acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc	1020
agcaccatcc aggtgttttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc	1080
caccaggggt gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac	1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac	1200
ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac ttctgaggac	1260
gtgccttttc acagcagcta cgtgcacagc cagagtttg acaggctgat gaatcctctc	1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc	1380
cagcagttgc tgttttctca ggcgggacct agcaacatgt cggctcaggc cagaaactgg	1440
ctgcctggac cctgtctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctgggtg	1560
aattcggggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgttttgcaa gcaggagct ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc	1800
caggggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt	1860
tgggccaaga ttctctcacac agatggcaac ttccaccctg ctcttttaac gggcggttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag	2100
attcagtata ctccaacta ctacaaatct acaaagtgg actttgctgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatggc actcgttacc ccaccgtaa tctgtaa	2217

<210> 18  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.52

<400> 18	
atggctgccg atggttatct tccagattgg ctgcaggaca acctctctga gggcattcgc	60
gagtgggtgg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagcagc agtcttccag	360
gccaaagaag gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaaga gaccggtaga gccgtacca cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca	540
gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgcctc tagtgtggga	600
tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac	660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctggggcctg cccacctaca acaaccacct ctacaagcaa	780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctacttttg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960

atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa tagcctcacc	1020
agcaccatcc aggtgttttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc	1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac	1140
ctgactccca acaacggtag tcaggccgtg ggacgttcct ctttctactg cctggagtac	1200
ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac ttctgaggac	1260
gtgcctttcc acagcagcta cgcgcacagc cagagtttg acaggctgat gaatcctctc	1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc	1380
cagcagttgc tgtcttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg	1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg	1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgtttggcaa gcaggagct ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc	1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacttgca gggctctatt	1860
tgggccaaga ttctcacac agatggcaac ttccaccgt ctcctttaat gggcggttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag	2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatggc actcgttacc tcaccgtaa tctgtaa	2217

<210> 19  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.46

<400> 19	
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtggtggg acctgaaacc tggagccccg aaaccctaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcac	480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca	540
gagtcagtcc ccgacctca acctatcgga gaacctccag cagcgccctc tagtgtggga	600
tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac	660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcacccgaac ctgggcccctg cccacctaca acaaccacct ctacaagcaa	780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag	900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960
atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc	1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc	1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac	1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct ctttctactg cctggagtac	1200
ttccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac	1260
gtgcctttcc acagcagcta cgcgcacagc cagagtgttg acaggctgat gaatcctctc	1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc	1380
cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg	1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg	1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgtttggcaa gcaggggagct ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaaggcc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc	1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt	1860
tgggccaaga ttctcacac agatggcaac ttccaccgt ctcctttaat gggcggtttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag	2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatgggc actcgttacc tcaccgtaa tctgtaa	2217

<210> 20  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.70

<400> 20	
atggctgccg atggttatct tccagattgg ctgaggaca acctctctga gggcattcgc	60
gagtgggtgg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaaagaag gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaaga gaccggtaga gccgtacca cagcgttccc ccgactcctc cacgggcattc	480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca	540
gagtcagtcc ccgacctca acctatcgga gaacctccag cagcgccctc tagtgtggga	600
tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac	660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctggggccctg cccgcctaca acaaccacct ctacaagcaa	780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tctcaccag tgactggcag	900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960
atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgcaa taacctcacc	1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc	1080
caccagggtc gcctgcctcc gttcccggcg gatgtcttca tgattcctca gtacggctac	1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct cttctactg cctggagtac	1200
ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac ttctgaggac	1260
gtgcctttcc acagcagcta cgcgcacagc cagagtttg acaggctgat gaatcctctc	1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc	1380
cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg	1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga gcggcagaga ctctctggtg	1560
aatccgggcy tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgtttggaac gcaggggagt ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataactaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc	1800
caggggagcct tacctggcat ggtctggcag aaccgggacg tgtacctga gggctctatt	1860
tgggccaaga ttctcacac agatggcaac ttccaccgt ctctttaat gggcggcttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tcttccatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagt ggagctgcag aaggagaaca gcaagcgtg gaaccagag	2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatggc actcgttacc tcaccgtaa tttgtaa	2217

<210> 21  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.61

<400> 21	
atggctgccg atggttatct tccagattgg ctgaggaca acctctctga gggcattcgc	60
gagtgggtgg acctgaaacc tggagccccg aaaccgaagg ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca	540
gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga	600
tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac	660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctggggcctg cccacctaca acaaccact ctacaagcaa	780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctacttttg ctacagcacc	840

ccctgggggt	attttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgacccatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccaggtca	aagaggtcac	gcagaatgaa	ggcaccaaga	ccatcgcaa	taacctcacc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagctgc	cgtacgtcct	cggtcttgcc	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttccctctct	agatgctgag	aacgggcaac	aacttttcct	tcagctaccc	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	acccagtcta	cgggaggcac	agcgggaacc	1380
cagcagttgc	tgttttctca	ggccgggcct	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgttacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccgggcg	tcgccatggc	aaccaacaag	gacgacgagg	accgcttctt	cccatccagc	1620
ggcatcctca	tgtttggaac	gcagggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaagac	accgctccta	ttgtgggggc	cgtcaacagc	1800
cagggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttcctcacac	agatggcaac	tttcacccgt	ctcctttaat	ggcggtttt	1920
ggacttaaac	atccgcctcc	tcaggtcctc	atcaaaaaca	ctcctgttcc	tgcggtcctt	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatca	cgcagtacag	caccggacaa	2040
gtcagcgtgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgtg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgctgt	taatactgag	2160
ggtgtttact	ctgagcctcg	ccccattggc	actcgttacc	tcacccgtaa	tctgtaa	2217

<210> 22  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.51

<400>	22					
atggttgccg	atggttatct	tccagattgg	ctcaggagaca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcagggc	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctta	aagcgggtga	caatccgtac	ctgcggtata	atcacgccga	cgccgagctt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaaagaag	gggttctcga	acctctcggt	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcatc	480
ggcaagaaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	acctatcgga	gaacctccag	cagcgccctc	tagtgtggga	600
tctggtacaa	tggctgcagg	cggtggcgcg	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcacccgaac	ctggggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctacttttg	ctacagcacc	840

ccctgggggt	atcttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aagagggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcacc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagctgc	cgtagctcct	cggtctgccc	1080
caccagggct	gccagcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttcccctctc	agatgctgag	aacgggcaac	aacttttcct	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtgttg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	acccagtcta	cgaggaggac	agcgggaacc	1380
cagcagttgc	tgttttctca	ggccgggcct	agcaacatgt	cggtcaggc	cagaaactgg	1440
ctgcctggac	cctgtacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctgggtg	1560
aatccgggcg	tcgccatggc	aaccaacaag	gacgacgagg	accgcttctt	cccatccagc	1620
ggcatcctca	tgtttgga	gcaggggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaac	accgctccta	ttgtgggggc	cgtaacagc	1800
cagggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttcctcacac	agatggcaac	tttcacccgt	ctcctttaat	ggcgggcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaca	ctcctgttcc	tgcggtatcct	1980
ccaacagcgt	tcaaccaggc	caagtgaat	tctttcatca	cgtagtacag	caccggacaa	2040
gtcagcgtgg	agatcgagtg	ggagccgcag	aaggagaaca	gcaagcgtg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgctgt	taatactgag	2160
ggtgtttact	ctgagcctcg	ccccattggc	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 23  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.50

<400>	23					
atggtgccc	atggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	atcacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaaagaagc	gggttctcga	acctctcggt	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaaag	gccagcagcc	cgccggaaag	agactcaatt	tcggtcagac	tggcgactca	540
gagtcagtcc	ccgacctca	acctatcgga	gaacctccag	cagcgccctc	tagtggtgga	600
tctggtacaa	tggtcgcagg	cggtggcgca	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcacccgaac	ctgggccctg	cccacctaca	acaaccacct	ctacaagcaa	780

atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctactttgg	ctacagcacc	840
ccctgggggt	atthttgactt	taacagattc	caetgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aagagggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcacc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagctgc	cgtacgtcct	cggtcttgcc	1080
caccagggtc	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttcccctctc	agatgctgag	aacgggcaac	aactttttct	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
gtcgaccagt	acctgtacta	cctgtcaaga	acccagtcta	cgggaggcac	agcgggaacc	1380
cagcagttgc	tgthtttctca	ggccgggcct	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccggggc	tcgccatggc	aaccaacaag	gacgacgagg	accgtttctt	cccatccagc	1620
ggcatcctca	tgthttggcaa	gcaggggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaaac	accgctccta	ttgtgggggc	cgtcaacagc	1800
cagggagcct	tacctggcat	ggctctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tggggccaaga	ttcctcacac	agatggcaac	tttcacccgt	ctcctttaat	ggcggtcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaca	ctcctgttcc	tgcggtatcct	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatca	cgcagtacag	caccggacaa	2040
gtcagcgtgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgtg	gagcccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgtctg	taatactgag	2160
ggtgtttact	ctgagcctcg	ccccattggc	actcgttacc	tcacccgtaa	tctgtaa	2217

<210> 24  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.39

<400> 24						
atggctgccg	atggttatct	tccagattgg	ctcaggagca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	atcacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggagcgc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggt	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcggac	tggcgactca	540
gagtcagtcc	ccgaccctca	acctatcgga	gaacctccag	cagcgccctc	tagtgtggga	600
tctggtacaa	tggctgcagg	cgggtggcga	ccaatggcag	acaataacga	aggtgccgac	660
ggagtggtga	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtt	720
atcaccacca	gcacccgaac	ctggggccctg	cccacctaca	acaaccacct	ctacaagcaa	780

atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctacttttg	ctacagcacc	840
ccctgggggt	atcttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aagagggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcgcc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagccgc	cgtacgtcct	cggtcttgcc	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttccccctctc	agatgctgag	aacgggcaac	aacttttcct	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	acccagtcta	cgggaggcac	agcgggaacc	1380
cagcagttgc	tgttttctcg	ggccgggcct	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgtacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccgggcg	tcgccatggc	aaccaacaag	gacgacgagg	accgcttctt	cccattccagc	1620
ggcatcctca	tgtttggaac	gcagggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaac	accgctccta	ctgtgggggc	cgtcaacagc	1800
cagggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttcctcacac	agatggcaac	tttcacccgt	ctcctttaat	gggcggcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaca	ctcctgttcc	tgcggtatcct	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatcg	cgcagtacag	caccggacaa	2040
gtcagcgtgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgtg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgcgg	actttgctgt	taatactgag	2160
ggtgtttact	ctgagcctcg	ccccattggc	actcgttacc	tcacccgtaa	tctgtaa	2217

<210> 25  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.49

<400>	25					
atggctgccg	atggttatct	tccagattgg	ctcaggagca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctgggtgct	tcctgggtac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgcac	ctgcggtata	atcacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggt	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcatac	480
ggcaagaaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	acttatcgga	gaacctccag	cagcgccttc	tagtgtggga	600
tctggtacaa	tggctgcagg	cggtggcgca	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720



atcaccacca	gcacccgaac	ctggggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
acctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctactttgg	ctacagcacc	840
ccctgggggt	attttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aagagggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcacc	1020
agcaccatcc	agggtgtttac	ggactcggaa	taccagctgc	cgtaactcct	cggctctgcc	1080
caccaggggt	gcctgcctcc	gttcccggcg	gacgtcttca	tgattctcta	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttccccctctc	agatgctgag	aacgggcaac	aacttttcct	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	acccagctta	cgggaggcac	agcgggaacc	1380
cagcagttgc	tgtttttctca	ggccgggcct	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccggggc	tcgccatggc	aaccaacaag	gacgacgagg	accgcttctt	cccattccagc	1620
ggcatctcta	tgtttgggcaa	gcagggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaaac	accgctccta	ttgtgggggc	cgtaacacagc	1800
caggggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttcctcacac	agatggcaac	tttcaccctg	ctcctttaat	gggcggcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaac	ctcctgttcc	tgcggtacct	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatca	cgcagtacag	caccggacaa	2040
gtcagcgcg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgctg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgctgt	taatactgag	2160
ggtgttttact	ctgagcctcg	ccccattggc	actcgttacc	tcaccggtaa	tctgtaa	2217

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcacccgaac ctggggccctg cccacctaca acaaccacct ctacaagcaa	780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960
atccaggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc	1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc	1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac	1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct ctttctactg cctggagtac	1200
ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac	1260
gtgccttttc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc	1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc	1380
cagcagctgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg	1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg	1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgttttgcaa gcaggggagt ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc	1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt	1860
tggggccaaga ttctctcacac agatggcaac ttccaccctg ctcctttaat gggcggttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaagca ctcctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagtgtg gaaccagag	2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgtgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatggc actcgttacc tcaccgtaa tctgtaa	2217

<210> 28  
 <211> 2196  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone pi.1

<400> 28	
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtgggtgg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag	360
gccaaaaaga gggactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag	480
cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc	540
caacctctct cagaaccacc cgcagggtccc tctggtctgg gatctggtac aatggctgct	600
ggcggtgggc ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca	660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg	720
acctggggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg	780
ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccttgggg gtattttgac	840
tttaacagat tccactgcca cttttcacca cgtgactggc agcgactcat caacaacaac	900
tgggggttcc ggccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc	960
accagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggctctt	1020
acggactcgg agtaccagct cccgtacgtg ctcggtctctg cccaccaggg ctgcctgcct	1080
ccgttcccg cggaactggt catgattccg cagtacgggt acctgacgct gaacaacggg	1140
agccaggccg tggggcgatc ctcttctac tgcctggagt actttccctc gcagatgctg	1200
agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc	1260
tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac	1320
tacctgtctc ggactcagac caacgggacc aatgccacgc agactctggt gtttgctcag	1380
gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggctc ttgctatcgg	1440
cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg	1500
gcgaccaagt accacctgaa cggccgagac tccctggtga gccccggtgt cgccatggca	1560
acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggaag	1620
cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag	1680
atcaagacca ccaaccctgt ggccacggag cagtacggcg tgggtggtga caatctgcag	1740
cagaccaact cagctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg	1800
gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg	1860
gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc	1920
cagatcctga tcaaaaacac gccggtacct gcggatcccc cgggtgaactt tacggacgct	1980
aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg	2040
gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat	2100
tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaacccgc	2160
cccattggca ctcgttacct caccgtaat ctgtaa	2196

<210> 29  
 <211> 2196  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone pi.3

<400> 29	
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtgggtgg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aaggggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caagagcgct tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag	360
gccaaaaaga gggactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag	480
ccgcgaaaa agagactgaa ttttgggccg actggcgact cagagtcagt gcctgacccc	540
caacctctct cagaaccacc tgcagggtccc tctggtctgg gatctggtac aatggctgca	600



ggcgggtggcg	ctccaatggc	agacaataac	gaaggcgccg	acggagtggg	taatgcctca	660
ggaaattggc	attgcgattc	cacatggctg	ggcgaccgag	tcataccac	cagcactcgg	720
acctggggccc	tccccaccta	caacaaccac	ctctacaagc	aaatctccaa	cgggacctcg	780
ggaggcgagca	gcaacgacaa	cacctacttt	ggctacagca	ccccctgggg	gtattttgac	840
tttaacagat	tccactgcc	cttttcacca	cgtgactggc	agcgactcat	caacaacaac	900
tgggggattcc	ggccaagag	gctcaacttc	aagctcttca	acatccaggt	caaggaggtc	960
accagaatg	aaggcaccaa	gaccatcgcc	aataacctca	ccagcacggt	gcaggctctt	1020
acggactcga	agtaccagct	cccgtacgtg	ctcggctctg	cccaccaggg	ctgcctgcct	1080
ccgttccccg	cggacgtgtt	catgattccg	cagtacgggt	acctgacgct	gaacaacggg	1140
agccaggccg	tggggcgatc	ctccttctac	tgcttgagg	actttccctc	gcagatgctg	1200
agaacgggca	acaactttac	cttcagctac	accttcgagg	acgtgccctt	ccacagcagc	1260
tacgcgcaca	gccagagcct	ggaccggctg	atgaacccgc	tgattgacca	gtacctgtac	1320
tacctgtctc	ggactcagac	caacgggacc	aatgccacgc	agactctgtt	gtttgctcag	1380
gccgggcctc	agaacatgtc	ggctcaggcc	aagaactggc	tgcttggtcc	ttgctatcgg	1440
cagcagcgcg	tctctacgac	agtgtcgcaa	aacaacaaca	gcaactttac	ctggaccggg	1500
gcgaccaagt	accacctgaa	cggccgagac	tccctggtga	accccggtgt	cgccatggca	1560
acgcacaagg	acgacgagga	gcgcttcttc	ccgagcagcg	gggtcctgat	gtttggcaag	1620
cagggcgctg	gaaaggacaa	tgtcgagtac	accaacgtga	tgctcaccag	cgaggaggag	1680
atcaagacca	ccaaccctgt	ggccacggag	cagtacgggt	tggtggctga	caatctgcag	1740
cagaccaact	cggctcccat	tgtgggggca	gtcaacagcc	agggggcctt	acccggtatg	1800
gtctggcaga	accgggacgt	gtacctgcag	ggtcccatct	gggccaagat	cccgcatacg	1860
gacggcaact	ttcaccgctc	tccttctcatg	ggcggctttg	gactgaaaca	cccgcctccc	1920
cagatcctga	tcaaaaacac	gccggtacct	gcggatcccc	cgggtgaactt	tacggacgct	1980
aagctggcga	gtttcatcac	gcagtacagc	accgggcagg	tcagcgtgga	gattgagtgg	2040
gagctgcaga	aggagaacag	caagcgctgg	aatcccgaga	ttcagtacac	ttccaattat	2100
tataaatcag	ctaattgtga	ctttgccgtc	aatgcagatg	gtgtatatag	tgaaccccg	2160
cccattggca	ctcgttacct	caccgtaat	ctgtaa			2196

<210> 31  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.60

<400> 31						
atggctgccg	atggttatct	tccagattgg	ctcaggagca	acctctctga	gggcattcac	60
gagtgggtggg	acccgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctgggtgct	tcctggctac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	atcacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcgg	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaagaaga	gaccggtaga	gccgtacca	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcagac	tggcgactca	540

gagtcagtcc	ccgaccctca	acctatcgga	gaacctccag	cagcgccctc	tagtgtggga	600
tctgtgtaca	tggctgcagg	cggtggcgca	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctggggccctg	cccaccacac	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaacg	tctacttcgg	ctacagcacc	840
ccctgggggt	attttgactt	caacagattc	cactgtcact	tctcaccacg	tgaccggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aagagggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcacc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagctgc	cgtacgtcct	cggtcttgcc	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcttca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttcccccttc	agatgctgag	aacgggcaac	aacttttcct	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	acccagtcta	cgggaaggcag	agcgggaacc	1380
cagcagttgc	tgttttctca	ggccgggcct	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccgggcg	tcgccatggc	aaccacaag	gacgacgagg	aacgcttctt	cccttcgagc	1620
ggagtctctga	tttttgaaaa	aactggagca	gctaataaga	ctacactgga	aaatgtgtta	1680
atgacaaatg	aagaggaaat	tcgtcctacc	aaccggtag	ccaccgagga	atacgggact	1740
gttagcagca	acctgcaggc	ggctaacact	gcagcccaga	cacaagttgt	caacaaccag	1800
ggagccttac	ctggtatggt	ctggcagaac	cgggacgtgt	acctgcaggg	tcccatctgg	1860
gccaagattc	ctcacacgga	cggcaacttt	caccgtctc	cgctgatggg	cggttttggg	1920
ctgaagcatc	ctcagatcct	gatcaaaaac	actcctgttc	ctgctaatacc	cccggagggtg	1980
tttacgcctg	ccaagtttgc	ttctttcatc	acacagtaca	gcaccggcca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaagcgct	ggaaccagga	gattcagtat	2100
acctccaatt	ttgacaaaca	gactgggtgtg	gactttgccg	ttgacagcca	gggtgtttat	2160
tctgagcctc	gccccattgg	tactcgttac	ctcaccgta	atctgtaa		2208

<210> 32  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.48

<400> 32						
atggctgctg	acggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtggtggg	acctgaaacc	tggagcccc	aagcccaagg	ccaaccagca	gaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcgagcgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcatc	480
ggcaagaaag	gccagcagcc	cgctagaaag	agactgaact	ttgggcagac	tggcgactca	540

gagtcagtc	ccgaccctca	accaatcgga	gaaccaccag	caggcccctc	tggctctgga	600
tctgtgtaca	tggctgcagg	cggtggcgca	ccaatggctg	acaataacaa	gggcgccgac	660
ggagtgggta	atgcctcagg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggctttg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccagtc	agtcagcagg	tagcaccaac	gacaacgtct	acttcggcta	cagcaccctc	840
tgggggtatt	ttgacttcaa	cagattccac	tgctacttct	caccacgtga	ctggcagcgg	900
ctcatcaaca	gcaactgggg	attccggccc	aagaagctca	acttcaagct	gttcaacatc	960
caggtaagg	aggtcacaac	gaatgacggc	gtcacgacca	tcgccaataa	ccttaccagc	1020
acgggttcagg	tcttttcgga	ctcgggaatac	cagctgcctt	acgtcctcgg	ctccgcacac	1080
cagggtctgc	tgccctcgtt	cccggcgagc	gtcttcatga	ttccccagta	cggtacctg	1140
actctgaaca	atggcagcca	atcggtgggt	cgcttctctt	tctactgcct	ggaatatattc	1200
cctttctcaa	tgctgagaac	gggcaacaac	ttcaccttca	gctacacctt	cgaggacggt	1260
cccttcacac	gcagctacgc	acacagccag	agcctggacc	ggctgatgaa	tcctcttatac	1320
gaccagtacc	tgtattacct	ggccagaaca	cagagcaacg	caggaggcac	agctggcaat	1380
cgggaactgc	agttttatca	gggcgggcct	accaccatgg	ccgaacaagc	caaaaactgg	1440
ctgcctggac	cttgcttccg	gcaacaaaga	gtctccaaga	cgctggatca	aaacaacaac	1500
agcaactttg	cttgactggg	tgccacaaa	taccatctaa	atggaagaaa	ttcattgggt	1560
aatcccggtg	tcgccatggc	aaccacaag	gacgacgagg	aacgcttctt	cccttcgagc	1620
ggagtcttga	tttttggaaa	aactggagca	gctaataaga	ctacactgga	aaatgtgtta	1680
atgacaaatg	aagaggaaat	tcgtcctacc	aaccggtag	ccaccgagga	atacgggact	1740
gttagcagca	acctgcaggc	ggctaacact	gcagcccaga	cacaagttgt	caacaaccag	1800
ggagccttac	ctggtatggg	ctggcagaac	cgggacgtgt	acctgcaggg	tcccatctgg	1860
gccaagattc	ctcacacgga	cggcaacttt	caccctcttc	cgctgatggg	cggcttttga	1920
ctgaagcatc	cgctcctca	gatcctgac	aaaaacactc	ctgttctctg	taatcccccg	1980
gagggtgtta	cgctgcaca	gtttgcttct	ttcatcacac	agtacagcac	cggccagggtc	2040
agcgtggaga	tcgagtggga	gctgcagaag	gagaacagca	agcgtgggaa	cccagagatt	2100
cagtatacct	ccaattttga	caaacagact	ggtgtggact	ttgccgttga	cagccagggt	2160
gtttattctg	agcctcgccc	cattgggtact	cgttacctca	cccgtaatct	gtaa	2214

<210> 33  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.62

<400>	33					
atggctgctg	acggttatct	tccagattgg	ctcaggagca	acctctctga	gggcattcgc	60
gagtggtggg	acctgaaacc	tggagcccc	aagcccaagg	ccaaccagca	gaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcgagcgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cggcgagttc	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcctccag	360
gccaagaagc	gggttctcga	acctctcggt	ctggctgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcac	480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gagccaccag caggccccctc tggctctggga	600
tctggtacaa tggctgcagg cgggtggcgca ccaatggctg acaataacaa gggcgccgac	660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa	780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc	840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg	900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc	960
cagggtcaagg aggtcacaac ggggtgacggc gtcacgacca tcgccataa ccttaccagc	1020
acgggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac	1080
cagggtctgac tgcctccgtt cccggcgagc gtcttcatga ttccccagta cggctacctg	1140
actctgaaca atgacagcca atcggtgggt cgttctctt tctactgcct ggaatatttc	1200
ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacggt	1260
cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttata	1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat	1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg	1440
ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac	1500
agcaactttt cttggactgg tgccacaaa taccatctaa atggaagaaa ttcattgggt	1560
aatcccggtg tcgccatggc aaccacaaag gacgacgagg aacgcttctt cccttcgagc	1620
ggagtccctga tttttgaaa aactggagca gctaataaga ctacactgga aaatgtgtta	1680
atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact	1740
gttagcagca acctgcaggc ggctaacct gcagcccaga cacaagttgt caacaaccag	1800
ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg	1860
gccaagattc ctcacacgga cggcaacttt caccctctc cgctgatggg cggctttgga	1920
ctgaagcatc cgctcctca gatctgatc aaaaacactc ctgttcctgc taatcccccg	1980
gaggtgttta cgctgcca gtttgcctt tcatcacac agtacagcac cggccaggtc	2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt	2100
cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt	2160
gtttattctg agcctcgccc cattggtact cgttacctca ccgtaatat gtaa	2214

<210> 34  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.44

<400> 34	
atggctgctg acggttatct tccagattgg ctgcaggaca acctctctga gggcattcgc	60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctgcgac	240
cagcggttca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct	420
ggaaagaagg gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac	480

ggcaagaaag gccagcagcc cgctagaaa agactgaact ttgggcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccctc tggctctggga	600
tctggtacaa tggctgcagg cgggtggcga ccaatggctg acaataacga gggcgccgac	660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gacccgaac ctgggctttg cccacctaca acaatcacct ctacaagcaa	780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc	840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg	900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc	960
caggtaagg aggtcacaa gaatgacggc gtcacgacca tcgccaataa ccttaccagc	1020
acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac	1080
cagggtgctc tgcctccgtt cccggcgagc gtcttcatga ttcccagta cggctacctg	1140
actctgaaca atggcagcca atcggtggtt cgttcctctt tctactgcct ggaatatttc	1200
ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt	1260
cccttcacac gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc	1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat	1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg	1440
ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac	1500
agcaactttg cttggactgg tgccacaaa taccatctaa atggaagaaa ttcattgggt	1560
aatcccggtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc	1620
ggagtctctg tttttgaaa aactggagca gctaataaga ctacactgga aaatgtgtta	1680
atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact	1740
gttagcagca acctgcaggc ggctaactac gcagcccaga cacaagttgt caacaaccag	1800
ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg	1860
gccaagattc ctcacacgga cggcaacttt caccgtctc cgctgatggg cggctttgga	1920
ctgaagcatc cgcctcctca gatcctgac aaaaacactc ctgttctctg taatcccccg	1980
gagggtgtta cgcctgccaa gtttgcttct ttcacacac agtacagcac cggccaggtc	2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt	2100
cagtatacct ccaattttga cgaacagact ggtgtggact ttgccgttga cagccagggt	2160
gtttattctg agcctcgccc cattgggtact cgttacctca cccgtaatct gtaa	2214

<210> 35  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.65

<400> 35	
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcttacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagcgc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct	420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccttc tggctctggga	600
tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac	660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa	780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc	840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg	900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc	960
cagggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc	1020
acgggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac	1080
cagggtctgcc tgcctccgtt cccggcggac gtcttcatga tttcccagta cggctacctg	1140
actctgaaca atggcagcca atcgggtgggt cgttcctctt tctactgcct ggaatatttc	1200
cctttctaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt	1260
cccttcacac gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc	1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat	1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg	1440
ctgcctagac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac	1500
agcaactttg cttggactgg tgccacaaa taccatctaa atggaagaaa ttcattgggt	1560
aatcccgtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc	1620
ggagtccctga tttttgaaa aactggagca gctaataaga ctacactgga aaatgtgtta	1680
atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact	1740
gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag	1800
ggagccttac ctggtatggc ctggcagaac cgggacgtgt acctgcaggg tcccatctgg	1860
gccaaagattc ctacacagga cggcaacttt caccgtctc cgctgatggg cggctttgga	1920
ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg	1980
gagggtgttta cgcctgccaa gtttgcttct ttcacacac agtacagcac cggccaggtc	2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt	2100
cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt	2160
gtttattctg agcctcggcc cattggtact cgttacctca cccgtaatct gtaa	2214

<210> 36  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.67

<400> 36	
atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc	60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accatgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcctccag	360
gccaagaagc gggttctcga acctctcggc ctggttgagg aagctgctaa gacggctcct	420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc caccggcatc	480
ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccctc tggctctggga	600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac	660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa	780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc	840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg	900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc	960
caggtaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ctttaccagc	1020
acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac	1080
cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg	1140
actctgaaca atggcagcca atcgggtgggt cgttcctctt tctactgcct ggaatatttc	1200
cctttctaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt	1260
cccttcacac gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatac	1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat	1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg	1440
ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac	1500
agcaactttg cttggactgg tgccacaaa taccatctaa atggaagaaa ttcattgggt	1560
aatcccgggt tgcctatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc	1620
ggagtcttga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta	1680
atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact	1740
gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag	1800
ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg	1860
gccaagattc ctcacacgga cggcaacttt caccctctc cgctgatggg cggctttgga	1920
ctgaagcatc cgcctcctca gatcctgac aaaaacactc ctgttcctgc taatcccccg	1980
gaggtgttta cgcctgccaa gtttgcttct ttcacacac agtacagcac cggccaggtc	2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt	2100
cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt	2160
gtttattctg agcctcgccc cattgggtact cgttacctca cccgtaatct gtaa	2214

<210> 37  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.55

<400> 37	
atggctgccg atggttatct tccagattgg ctgcaggaca acctctctga gggcattcgc	60
gagtgggtggg acctgaaacc tggagccccg aaaccctaaag ccaaccagca aaagcaggac	120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360

gccaaagaagc	gggttctcga	acctctcggg	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcatc	480
ggcaagaaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	acctatcggg	gaacctccag	cagcgccctc	tagtgtggga	600
tctggtacaa	tggctgcagg	cgggtggcga	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	cacggctggg	cgacagagtc	720
atcaccacca	gcacccgga	ctgggctttg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccagtc	agtcagcagg	tagcaccaac	gacaacgtct	acttcggcta	cagcaccctc	840
tgggggtatt	ttgacttcaa	cagattccac	tgctacttct	caccacgtga	ctggcagcgg	900
ctcatcaaca	acaactgggg	attccggccc	aagaagctca	acttcaagct	gttcaacatc	960
cagggtcaagg	aggtcacca	gaatgacggc	gtcacgacca	tcgccaataa	ccttaccagc	1020
acgggttcagg	tcttttcgga	ctcgggaatac	cagctgccct	acgtcctcgg	ctccgcacac	1080
cagggtctgcc	tgctctcgtt	cccggcggac	gtcttcatga	ttcccagta	cggctacctg	1140
actctgaaca	atggcagcca	atcgggtggg	cgcttctctt	tctactgcct	ggaatatttc	1200
ccttctcaaa	tgctgagaac	gggcaacaac	ttcaccttca	gctacacctt	cgaggacggt	1260
ccctccaca	gcagctacgc	acacagccag	agcctggacc	ggctgatgaa	tcctcttata	1320
gaccagtacc	tgtattacct	ggccagaaca	cagagcaacg	caggaggcac	agctggcaat	1380
cgggaactgc	agttttatca	gggcgggcct	accaccatgg	ccgaacaagc	caaaaactgg	1440
ctgcctggac	cttgcttccg	gcaacgaaga	gtctccaaga	cgctggatca	aaacaacaac	1500
agcaactttg	cttggactgg	tgccacaaaa	taccatctaa	atggaagaaa	ttcattgggt	1560
aatcccggtg	tcgccatggc	aaccacaaag	gacgacgagg	aacgcttctt	cccttcgagc	1620
ggagtctctga	tttttgaaaa	aactggagca	gctaataaga	ctacactgga	aaatgtgtta	1680
atgacaaatg	aagaggaaat	tcgtcctacc	aaccggtag	ccaccgagga	atacgggact	1740
gttagcagca	acctgcaggc	ggctaacact	gcagcccaga	cacaagtgtg	caacaaccag	1800
ggagccttac	ctggtatggg	ctggcagaac	cgggacgtgt	acctgcaggg	tcccatctgg	1860
gccaagattc	ctcacacgga	cggcaacttt	caccgtctc	cgctgatggg	cggctttgga	1920
ctgaagcatc	cgctcctca	gatcctgac	aaaaaactc	ctgttctcgc	taatcccccg	1980
gaggtgttta	cgctgcca	gtttgcttct	ttcatcacac	agtacagcac	cggccaggtc	2040
agcgtggaga	tcgagtggga	gctgcagaag	gagaacagca	agcgtgggaa	cccagagatt	2100
cagtatacct	ccaattttga	caaacagact	ggtgtggact	ttgccgttga	cagccagggt	2160
gtttattctg	agcctcgccc	cattgggtact	cgttacctca	cccgtaatct	gtaa	2214

<210> 38  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.47

<400>	38	
atggctgccg	atggttatct	tccagattgg
gagtggtggg	acctgaaacc	tggagccccg
gacggccggg	gtctggtgct	tcctggctac
aagggggagc	ccgtcaacgc	ggcggacgca
cagcagctca	aagcgggtga	caatccgtac
caggagcgtc	tgcaagaaga	tacgtctttt
	gggggcaacc	tcgggcgagc
	agtcctccag	
		60
		120
		180
		240
		300
		360

gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcatc	480
ggcaagaaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	acctatcgga	gaacctccag	cagcgccctc	tagtgtggga	600
tctggtacaa	tggctgcagg	cgggtggcga	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggcccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctactttgg	ctacagcacc	840
ccctgggggt	attttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccaggcca	aagaggccac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taaccttacc	1020
agcacgggtc	aggtcttttc	ggactcgga	taccagctgc	cctacgtcct	cggtccgca	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcccca	gtacggctac	1140
ctgactctga	acaatggcag	ccaatcgggtg	ggtcgttcct	ctttctactg	cctggaatat	1200
ttcccttctc	aaatgctgag	aacgggcaac	aacttcacct	tcagctacac	cttcgaggac	1260
gttcccttcc	acagcagcta	cgcacacagc	cagagcctgg	accggctgat	gaatcctctt	1320
atcgaccagt	acctgtatta	cctggccaga	acacagagca	acgcaggagg	cacagctggc	1380
aatcgggaac	tgagttttta	tcaggggcggg	cctaccacca	tggccgaaca	agccaaaaac	1440
tggctgcctg	gaccttgctt	ccggcaacaa	agagtctcca	agacgctgga	tcaaaacaac	1500
aacagcaact	ttgcttggac	tgggtgccacc	aaataccatc	taaatggaag	aaattcattg	1560
gttaatcccc	gtgtcgccat	ggcaaccac	aaggacgacg	aggaacgctt	cttcccttcg	1620
agcggagtcc	tgatttttgg	aaaaactgga	gcagctaata	agactacact	ggaaaatgtg	1680
ttaatgacaa	atgaagagga	aattcgctct	accaacccgg	tagccaccga	ggaatacggg	1740
actgttagca	gcaacctgca	ggcggctaac	actgcagccc	agacacaagt	tgtcaacaac	1800
caggagcct	tacctgggtat	ggctctggcag	aaccgggacg	tgtacctgca	gggtcccatc	1860
tgggccaaga	ttctcacac	ggacggcaac	tttcacccgt	ctccgctgat	ggcggtctt	1920
ggactgaagc	atccgcctcc	tcagatcctg	atcaaaaaca	ctcctgttcc	tgctaataccc	1980
ccggagggtg	ttacgcctgc	caagtttgct	tctttcatca	cacagtacag	caccggccag	2040
gtcagcgtgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgtg	gaaccagag	2100
attcagtata	cctccaattt	tgacaaacag	actggtgtgg	actttgccgt	tgacagccag	2160
ggtgtttatt	ctgagcctcg	ccccattggt	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 39  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.69

<400> 39						
atggctgctg	acggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagcccc	aagcccaagg	ccaaccagca	gaagcaggac	120
gacggccggg	gtctgggtgct	tcctggctac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgccgagttt	300

caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggagagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcgg	ctggttgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcatc	480
ggcaagaaag	gccagcagcc	cgctagaaag	agactgaact	ttgggcagac	tggcgactca	540
gagtcagtcc	ccgaccctca	accaatcgga	gaaccaccag	caggccccctc	tggctctggga	600
tctggtacaa	tggctgcagg	cggtggcgcc	ccaatggcag	acaataacga	aggcgccgac	660
ggagtgggta	atgcctcagg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggctttg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccagtc	agtcagcagg	tagcaccaac	gacaacgtct	acttcggcta	cagcaccccc	840
tgggggtatt	ttgacttcaa	cagattccac	tgtcacttct	caccacgtga	ctggcagcgg	900
ctcatcaaca	acaactgggg	attccggccc	aagaagctca	acttcaagct	gttcaacatc	960
caggtaaggg	aggtcacaac	gaatgacggc	gtcacgacca	tcgccaataa	ccttaccagc	1020
acgggttcagg	tcttttcgga	ctcgggaatac	cagctgccct	acgtcctcgg	ctccgcacac	1080
cagggctgcc	tgcctccgtt	cccggcggaac	gtcttcatga	ttccccagta	cggctacctg	1140
actctgaaca	atggcagcca	atcgggtgggt	cgttcctctt	tctactgcct	ggaatatttc	1200
cctttctcaa	tgctgagaac	gggcaacaac	ttcaccatca	gctacacctt	cgaggacggt	1260
cccttccaca	gcagctacgc	acacagccag	agcctggacc	ggctgatgaa	tcctcttatc	1320
gaccagtacc	tgtattacct	ggccagaaca	cagagcaacg	caggaggcac	agctggcaat	1380
caggaaactgc	agttttatca	gggcgggcct	accaccatgg	ccgaacaagc	caaaaactgg	1440
ctgcctggac	cttgcttccg	gcaacaaaga	gtctccaaga	cgctggatca	aaacaacaac	1500
agcaactttg	cttggaactgg	tgccaccaaa	taccatctaa	atggaagaaa	ttcattgggt	1560
aatcccggtg	tcgccatggc	aaccacaaag	gacgacgagg	aacgcttctt	cccttcgagc	1620
ggagtctctga	tttttggaag	aactggagca	gctaataaga	ctacactgga	aaatgtgtta	1680
atgacaaatg	aagaggaaat	tcgtcctacc	aaccggtag	ccaccgagga	atacgggact	1740
gttagcagca	acctgcaggc	ggctaacact	gcagcccaga	cacaagttgt	caacaaccag	1800
ggagccttac	ctggtatgg	ctggcagaac	cgggacgtgt	acctgcaggg	tcccactctg	1860
gccaagattc	ctcacacaga	tggcaacttt	caccgtctc	ctttaatggg	cggctttgga	1920
cttaaacatc	cgctcctca	gatcctcacc	aaaaaactc	ctgttctctg	ggatcctcca	1980
acagcgttca	accaggccaa	gctgaattct	ttcatcacgc	agtacagcac	cggacaagtc	2040
agcgtggaga	tcgagtggga	gctgcagaag	gagaacagca	agcgtgggaa	cccagagatt	2100
cagtatactt	ccaactacta	caaactctaca	aatgtggact	ttgctgttaa	tactgagggt	2160
gtttactctg	agcctcgccc	cattggcact	cgttacctca	cccgtaactc	gtaa	2214

<210> 40  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.54

<400>	40	
atggctgctg	acggttatct	tccagattgg
gagtggtggg	acctgaaacc	tggagccccg
gacggccggg	gtctggtgct	tcctggctac
aagggggagc	ccgtcaacgc	ggcgagcgca
cagcagctca	aagcgggtga	caatccgtac
		ctgcggtata
		accacgccga
		cgccgagttt
		60
		120
		180
		240
		300

caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaaag	gccagcagcc	cgctagaaag	agactgaact	ttgggcagac	tggcgactca	540
gagtcagtc	ccgaccctca	acctctcggg	gaaccaccag	caggcccctc	tggctcggga	600
tctggtacaa	tggctgcagg	cgggtggcgt	ccaatggcag	acaataacga	aggcgccgac	660
ggagtgggta	atgcctcagg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggctttg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccagtc	agtcagcagg	tagcaccaac	gacaacgtct	acttcggcta	cagcaccctc	840
tgggggtatt	ttgacttcaa	cagattccac	tgtcacttct	caccacgtga	ctggcagcga	900
ctcatcaaca	acaactgggg	attccggccc	aagaagctca	acttcaagct	cttcaacatc	960
caagtcaagg	aggctacgac	gaatgacggc	gtcacgacca	tcgctaataa	ccttaccagc	1020
acgggttcagg	tcttttcgga	ctcggagtag	cagctgccgt	acgtcctcgg	ctctgcccac	1080
cagggtctgc	tgcctccgtt	cccggcggac	gtcttcatga	ttcctcagta	cggctacctg	1140
actctgaaca	atggcagcca	atcgggtggg	cggtcatcct	tctactgcct	ggaatacttc	1200
ccttctcagg	tgctgagaac	gggtaacaac	ttcaccttca	gttacacctt	cgaggacgtg	1260
cctttccaca	gcagctacgc	gcacagccag	agcctagacc	ggctgatgaa	tcccctcatc	1320
gaccagtacc	tgtattacct	ggctagaaca	cagagtaacc	caggaggcac	atctggcaat	1380
cgggaactgc	agttttacca	gggcgggcct	tccaccatgg	ccgaacaagc	caagaactgg	1440
ttacctggac	cttgcttccg	gcaacaaaga	gtttccaaaa	cactggatca	aaacaacaac	1500
agcaactttg	cttggactgg	tgccacaaaa	tatcacctga	acggcagaaa	ctcattgggtg	1560
aatcctgggt	tcgccatggc	aactcacaag	gacgacgagg	accgcttttt	cccattccagc	1620
ggagtctctga	tttttgga	aactggagca	accaacaaga	ctacattgga	aaacgtgtta	1680
atgacaaatg	aagaagaaat	tcgtcctact	aatcctgtgg	ccacagaaga	atacgggata	1740
gtcagcagca	atttacaagc	ggccaatact	gcagcccaga	cacaagttgt	caacaaccag	1800
ggagccttac	ctggcatggg	ctggcagaac	cgggacgtgt	acctgcaggg	tcccatctgg	1860
gccaaaattc	ctcacacaga	cggcaacttt	caccgtcttc	cgctgatggg	cggctttgga	1920
ctgaagcatc	cgctcctca	gacctgatc	aaaaaacttc	ctgttcctgc	taatcccccg	1980
gaggtgttta	cgcttgccaa	gtttgcttct	ttcatcacac	agtacagcac	cggccagggtc	2040
agcgtggaga	tcgagtggga	gctgcagaag	gagaacagca	agcgtgggaa	cccagagatt	2100
cagtatacct	ccaattttga	caaacagact	ggtgtggact	ttgccgttga	cagccagggt	2160
gtttattctg	agcctcgccc	cattgggtact	cgttacctca	cccgtaatct	gtaa	2214

<210> 41  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.45

<400> 41						
atggctgccg	atggttatct	tccagattgg	ctcaggagca	acctctctga	gggcattcgc	60
gagtggtggg	acctgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct	420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac	480
ggcaagaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccccctc tggctctggga	600
tctggtacaa tggctgcagg cgggtggcgct ccaatggcag acaataacga aggcgcgcgac	660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctgggcctttg cccacctaca acaaccacct ctacaagcaa	780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc	840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg	900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc	960
caggtaagg aggtcacac gaatgacggc gtcacgacca tcgccaataa ccttaccagc	1020
acgggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac	1080
cagggtctgc tgcctccgtt cccggcgac gtcttcatga ttcctcagta cggctacctg	1140
acttcaaca acggtagtca ggccgtggga cgttctcct tctactgcct ggagtacttc	1200
ccctctcaga tgctgagaac gggcaacaac ttttcttca gctacacttt cgaggacgtg	1260
cctttccaca gcagctacgc gcacagccag agtttggaac ggctgatgaa tcctctcatc	1320
gaccagtacc tgtactacct gtcaagaacc cagttctacg gaggcacagc gggaaccag	1380
cagttgctgt tttctcaggc cgggcctagc aacatgtcga ctcaggccag aaactggctg	1440
cctggaccct gctacagaca gcagcgcgtc tccacgacac tgtcgcaaaa caacaacagc	1500
aactttgcct ggactgggtgc caccaagtat catctgaacg gcagagactc tctggtgaat	1560
ccgggcgtgc ccatggcaac caacaaggac gacgaggacc gcttcttccc atccagcggc	1620
atcctcatgt ttggcaagca gggagctgga aaagacaacg tggactatag caacgtgatg	1680
ctaaccagcg aggaagaaat caagaccacc aaccccgtag ccacagaaca gtatggcgtg	1740
gtggctgata acctacagca gcaaacacc gctcctattg tgggggccgt caacagccag	1800
ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatttgg	1860
gccaagattc ctacacaga tggcaacttt caccctctc ctttaatggg cggctttgga	1920
cttaaacatc cgctcctca gatccttacc aaaaacactc ctgttcctgc ggatcctcca	1980
acagcgttca accaggccaa gctgaattct tcatcacgc agtacagcac cggacaagtc	2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt	2100
cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgaggg	2160
gcttactctg agcctcgccc cattggcact cgttacctca cccgtaactc gtaa	2214

<210> 42  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.59

<400> 42	
atggctgctg acggttatct tccagattgg ctgcaggaca acctctctga gggcattcgc	60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct	420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca	540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccccctc tggcttgga	600
tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac	660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa	780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc	840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg	900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc	960
cagggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccataa ccctaccagc	1020
acgggtcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac	1080
cagggctgcc tgcctcgggt cccggcggaac gtcttcatga ttccccagta cggctacctg	1140
actctgaaca atggcagcca atcgggtggg cgttcctctt tctactgcct ggaatatctc	1200
ccttctcaaa tgctgagaac gggcaacaac ttcacctca gctacacctt cgaggacgtt	1260
cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc	1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat	1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg	1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg	1560
aatccgggagc tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgttttgcaa gcaggagct ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc	1800
cagggagcct tacctggcat ggtctggcag aaccgggagc tgtacctgca gggctctatt	1860
tgggccaaga ttcttcacac agatggcaac ttccaccgt ctctttaa gggcggtttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag	2100
attcagtata cttccaacta ctacaaatct acaaagtgg actttgctgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatggc actcgttacc tcaccgtaa tctgtaa	2217

<210> 43  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.43

<400> 43	
atggctgccg atggttatct tccagattgg ctgcaggaca acctctctga gggcattcgc	60
gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac	120
gacggccggg gcctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180

```

aagggggagc ccgtaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480
aagaaaggcc aacagcccg cagaaaaaga ctcaattttg gccagactgg cgactcagag 540
tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600
aatacaatgg ctgcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctggcgga cagagtcac 720
accaccagca cccgaacctg ggcctgccc acctacaaca accacctcta caagcaaatac 780
tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagaccccc 840
tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900
ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960
caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020
accatccagg tgtttacgga ctcggtac cagctgccgt acgttctcgg ctctgcccac 1080
cagggtgccc tgcctccgtt cccggcggac gtgttcatga ttcccagta cggctaccta 1140
aactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200
ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260
cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320
gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgag 1380
actctgggct tcagccaagg tgggcctaata caaatggcca atcaggcaaa gaactggctg 1440
ccaggacctt gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500
aactttgcct ggactgctgg gaccaataac catctgaatg gaagaaattc attggctaata 1560
cctggcatcg ctatggcaac acacaagac gacgaggagc gttttttccc agtaacggga 1620
tcctgttttt ggcaacaaaa tgctgccaga gacaatgcgg attacagcga tgctatgctc 1680
accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740
gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800
gccttaccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggccc 1860
aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920
aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980
accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040
gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100
tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160
tactctgaac cccgccccat tggcaccctg tacctcacc gtaatctgta a 2211

```

```

<210> 44
<211> 2211
<212> DNA
<213> Unknown

```

```

<220>
<223> new AAV serotype, clone hu.3

```

```

<400> 44
atggctgccg atggttatct tccagattgg ctgcaggaca ctctctctga aggaataaga 60
cagtggtgga agctcaaacc tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

```

aagggggagc	cggtaacga	ggcagacgcc	gcggccctcg	agcacgacaa	ggcctacgac	240
cggcagctcg	acagcggaga	caaccgtac	ctcaagtaca	accacgccga	cgcagagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcgaaaaaga	gggttcttga	acctctgcgg	cctggtttga	ggaaacctgt	taagacggct	420
ccgggaaaaa	agaggccggt	agagcactct	cctgtggagc	cagactcctc	ctcgggaacc	480
ggaaaagcgg	gccagcagcc	tgcaagaaaa	agattaaatt	ttggtcagac	tgagacgca	540
gactccgtac	ctgaccccca	gcctctcgga	cagccaccag	cagccccctc	tggtctggga	600
tctactacaa	tggtctacag	cagtggcgca	ccaatggcag	acaataacga	gggtgccgat	660
ggagtgggta	attcctcagg	aaattggcat	tgcgattccc	aatggctgga	cgacagagtc	720
atcgccacca	gcaccgaac	ctgggcccctg	cccacataca	acaaccacct	ctacaagcaa	780
atctccagcc	aatcaggagc	ctgcaacgac	aaccactact	ttggctacag	cacccccctg	840
gggtattttt	acttcaacag	attccactgc	cactttttcac	cacgtgactg	gcaaagactc	900
atcaacagca	actggggatt	ccggcccaaa	agactcaact	tcaagctctt	taatattcaa	960
gtcaaagagg	tcacgcagaa	tgacggtacg	acgacgattg	ccaataacct	taccagcacg	1020
gttcagggtg	ttactgactc	ggagtaccag	ctcccgtacg	tcccgggctc	ggcgcatcaa	1080
ggatgcctcc	cgccgtttcc	agcggacgtc	ttcatgggtc	cacagtatgg	atacctcacc	1140
ctgaacaacg	ggagtccagg	ggtaggacgc	tcttcctttt	actgcctgga	gtactttcct	1200
tctcagatgc	tgctacttgg	aaacaacttt	cagttcagct	acacttttga	agacgtgcct	1260
ttccacagca	gctacgctca	ctgccagagt	ctggatcggc	tgatgaatcc	tctgatcgac	1320
cagtacctgt	attatctgaa	caagacacaa	acaaatagt	gaactcttca	gcagtctcgg	1380
ctactgttta	gccaagctgg	accaaccaac	atgtctcttc	aagctaaaaa	ctggctgcct	1440
ggaccttgct	acagacagca	gcgtctgtca	aaacaggcaa	acgacaataa	caactgcaac	1500
tttccctgga	ctgcagctac	aaagtatcat	ctaaatggcc	gggactcgtt	ggttaatcca	1560
ggaccagcta	tggtccagtca	caaggatgac	gaagaaaagt	ttttcccat	gcatggaacc	1620
ctgatatttg	gtaaacagg	aacaaatgcc	aacgacgcgg	atttggaata	tgatcatgatt	1680
acagatgaag	aagaaatcag	gcccaccaat	cccgtggcta	cggagcagta	cgggactgtg	1740
tcaataaatt	tgcaaaactc	aaacactggt	ccaactacag	gaactgtcaa	tcaccaagga	1800
gcgttacctg	gtatgggtg	gcaggatcga	gacgtgtacc	tgacgggacc	catttggggc	1860
aagattcctc	acaccgatgg	acactttcat	ccttctccac	tgatgggagg	ttttggactc	1920
aaacaccgc	ctcctcagat	catgatcaaa	agcactccc	ttccagccaa	tcctcccaca	1980
aacttcagtt	ctgccaagtt	tgcttcttcc	atcacacagt	attccacggg	acaggtcagc	2040
gtggagatcg	agtgggagct	gcagaaggag	aacagcaaac	gctggaatcc	cgaaattcag	2100
tacacttcca	actacaacaa	gtctgttaat	gtggacttta	ctgtggacac	taatggtgtg	2160
tattcagagc	ctcgccccat	tggcaccaga	tactgactc	gtaatctgta	a	2211

<210> 45  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.5

<400>	45	
atggctgccg	atggttatct	tccagattgg
ctcgaggaca	ctctctctga	aggaataaga
		60
cagtgggtgga	agctcaaacc	tggtccacca
ccaccaaaagc	ccgcagagcg	gcataaggac
		120

gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	cggtaacga	ggcagacgcc	gcggccctcg	agcacgacaa	ggcctacgac	240
cggcagctcg	acagcggaga	caaccctgac	ctcaagtaca	accacgccga	cgcagagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcgaaaaaga	gggttcttga	acctctgggc	ctggttgagg	aacctgttaa	gacgggtccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
aaagcgggcc	agcagcctgc	aagaaaaaga	ttaaattttg	gtcagactgg	agacgcagac	540
tccgtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggatct	600
actacaatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgaggg	tgccgatgga	660
gtgggttaatt	cctcaggaaa	ttggcattgc	gattcccaat	ggctgggcga	cagagtcatc	720
accaccagca	cccgaacctg	ggccctgccc	acatacaaca	accacctcta	caagcaaatc	780
tccagccaat	caggagccag	caacgacaac	cactactttg	gctacagcac	cccctggggg	840
tattttgact	tcaacagatt	ccactgccac	ttttcaccac	gtgactggca	aagactcatc	900
aacaacaact	ggggattccg	gccccaaaaga	ctcaacttca	agctctttaa	tattcaagtc	960
aaagaggta	cgcagaatga	cggtagcgac	acgattgcca	ataaccttac	cagcacggtt	1020
cagggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tgggctcggc	gcatcaagga	1080
tgcctcccgc	cgtttccagc	ggacgtcttc	atgggtccac	agtatggata	cctcacctcg	1140
aacaacggga	gtcaggcggt	aggacgtctc	tccttttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtactggaaa	caactttcag	ttcagctaca	cttttgaaga	cgtgcctttc	1260
cacagcagct	acgtcacag	ccagagtctg	gatcggctga	tgaatcctct	gatcgaccag	1320
tacctgtatt	atctgaacaa	gacacaaaca	aatagtggaa	ctcttcagca	gtctcggcta	1380
ctgtttagcc	aagctggacc	aaccaacatg	tctcttcaag	ctaaaaactg	gctgcctgga	1440
ccttgctaca	gacagcagcg	tctgtcaaaa	caggcaaacg	acaacaacaa	cagcaacttt	1500
ccctgggactg	cagctacaaa	gtatcatcta	aatggccggg	actcgttggg	taatccagga	1560
ccagctatgg	ccagtcgcaa	ggatgacgaa	gaaaagtgtt	tccccatgca	tggaaacctg	1620
atattttgga	aacaaggaac	aaatgccaac	gacgcggatt	tggaaaaatg	catgattaca	1680
gatgaagaag	aaatcagggc	caccaatccc	gtggctacgg	agcagtagcg	gactgtgtca	1740
aataatttgc	aaaactcaaa	cactggtcca	actactggaa	ctgtcaatca	ccaaggagcg	1800
ttacctggga	tgggtgtggca	ggatcgagac	gtgtacctgc	agggaccat	ttgggccaag	1860
attcctcaca	ccgatggaca	ctttcatcct	tctccactga	tgggaggttt	tggactcaaa	1920
caccgcctc	ctcagatcat	gatcaaaaac	actcccgttc	cagccaatcc	tcccacaaac	1980
ttcagttctg	ccaagtttgc	ttctttcatc	acacagtatt	ccacgggaca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	aattcagtac	2100
acttccaact	acaacaagtc	tgttaatgtg	gactttactg	tggacactaa	tgggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 46  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.1

<400>	46	
atggctgccc	atggttatct	tccagattgg
ctcgaggaca	ctctctctga	aggaataaga
		60
cagtgggtgga	agctcaaac	tggcccacca
ccaccaaac	ccgcagagcg	gcataaggac
		120

gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	cggtaacga	ggcagacgcc	gcggccctcg	agcacgacaa	ggcctacgac	240
cggcagctcg	acagcggaga	caaccggtac	ctcaagtaca	accacgccga	cgcagagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcgaaaaaga	gggttcttga	acctctgggc	ctgggtgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
aaagcgggcc	agcagcctgc	aagaaaaaga	ttaaattttg	gtcagactgg	agacgcagac	540
tccgtacctg	accccgagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggatct	600
actacaatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgaggg	tgccgatgga	660
gtgggtaatt	cctcaggaaa	ttggcattgc	gattcccaat	ggctgggcga	cagagtcata	720
accaccagca	cccgaacctg	ggccctgccc	acatacaaca	accacctcta	caagcaaatc	780
tccagccaat	caggagccag	caacgacaac	cactactttg	gctacagcac	cccctggggg	840
tattttgact	tcaacagatt	ccactgccac	ttttcaccac	gtgactggca	aagactcatc	900
aacaacaact	ggggattccg	gccccaaaaga	ctcaacttca	agctctttaa	tattcaagtc	960
aaagagggtca	cgcagaatgg	cggtagcagc	acgattgccca	ataaccttac	cagcacgggt	1020
cagggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tgggctcggc	gcatcaagga	1080
tgcctcccgc	cgtttccagc	ggacgtcttc	atgggtccac	agtatggata	cctcacctcg	1140
aacaacggga	gtcaggcggg	aggacgtctt	tccttttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtactggaaa	caactttcag	ttcagctaca	cttttgaaga	cgtgcctttc	1260
cacagcagct	acgtcacag	ccagagtctg	gatcggctga	tgaatcctct	gatcgaccag	1320
tacctgtatt	atctgaacaa	gacacaaaca	aatagtggaa	ctcttcagca	gtctcggcta	1380
ctgttttagcc	aagctggacc	aaccaacatg	tctcttcaag	ctaaaaactg	gctgcctgga	1440
ccttgctaca	gacagcagcg	tctgtcaaaa	caggcaaacg	gcaacaacaa	cagcaacttt	1500
ccctggactg	cagctacaaa	gtatcatcta	aatggccggg	actcgttggg	taatccagga	1560
ccagctatgg	ccagtcacaa	ggatgacgaa	gaaaagtgtt	tccccatgca	tggaaccctg	1620
atattttgga	aacaaggaac	aaatgccaac	gacgcgggatt	tggaaaatgt	catgattaca	1680
gatgaagaag	aaatcagggc	caccaatccc	gtggctacgg	agcagtacgg	gactgtgtca	1740
aataatttgc	aaaactcaaa	cactgggtcca	actactggaa	ctgtcaatca	ccaaggagcg	1800
ttacctggta	tgggtgtggca	ggatcgagac	gtgtacctgc	agggacccat	ttgggccaag	1860
attcctcaca	ccgatggaca	ctttcatcct	tctccactga	cgggagggtt	tggactcaaa	1920
caccgcctc	ctcagatcat	gatcaaaaac	actcccgttc	cagccaatcc	tcccacaaac	1980
ttcagttctg	ccaagtttgc	ttctttcatc	acacagtatt	ccacgggaca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatccccga	aattcagtac	2100
acttccaact	acaacaagtc	tgtaaatgtg	gactttactg	tggacactaa	tgggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 47  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.4

<400>	47	
atggctgccc	atggttatct	tccagattgg
ctcgaggaca	ctctctctga	aggaataaga
		60

cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac	180
aagggggagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggccacgac	240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctgggtgagg agcctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac	540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggatct	600
actacaatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg tgccgatgga	660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctggcgga cagagtcatc	720
accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatac	780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg	840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcgtc	900
aacaacaacc ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc	960
aaagaggcca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga	1080
tgcctcccgc cgtttccagc ggacgtcttc atgggtccac agtatggata cctcaccctg	1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttctt	1200
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc	1260
cacagcagct acgctcacag ccagagtctg gatcggtgga tgaatcctct gatcgaccag	1320
tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta	1380
ctgttttagc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga	1440
ccttgctaca gacagcagcg tctgtcaaaa caggcaaagc acaacaaca cagcaacttt	1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga	1560
ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg	1620
atattttgga aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca	1680
gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca	1740
aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatca ccaaggagcg	1800
ttacctgga tggtgtggca ggcagcagac gtgtacctgc agggacccat ttgggccaag	1860
attcctcaca ccgatggaca ctttcacatc tctccactga tgggaggttt tggactcaaa	1920
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac	1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tgggtgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 48  
 <211> 2209  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.2

<400> 48	
atggctgccg atggttatcc tccagattgg ctgcaggaca ctctctctga agggataaga	60

cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac	180
aagggggagc cggccaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcagagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcggcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac	540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct	600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga	660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac	720
accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaadc	780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg	840
tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc	960
aaagaggta cgcagaatga cggtagcagc acgattgccataaaccttac cagcacggtt	1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga	1080
tgcctcccg cgtttccagc ggacgtcttc atgggtccac agtatggata cctcaccctg	1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct	1200
cagatgtgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc	1260
cacagcagct acgctcacag ccagagtctg gatcggtga tgaatcctt gatcgaccag	1320
tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggtta	1380
ctgttttagc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga	1440
ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt	1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga	1560
ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg	1620
atatttggt aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca	1680
gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtagcg gactgtgtca	1740
aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatcg ccaaggagcg	1800
ttacctggt tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag	1860
attcctcaca ccgatggaca ctttcacatc tctccactga tgggagggtt tggactcaaa	1920
caccgcctc ctcatgcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac	1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat	2160
tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaat	2209

<210> 49  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.25

<400> 49

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgtgtga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac	120
ggcagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctca acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg	420
ggaaaaaaga gaccggtaga gcaactctct gcggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac	540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggatct	600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga	660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcca cagagtcac	720
accacaagca ctcgaaacct ggccctgccc acctacaaca accacctcta caagcaaatc	780
tccagccaat caggagcctc aaacgacaac cactattttg gctacagcac cccttggggg	840
tattttgact tcaacagatt ccaactgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagaggcca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt	1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccg cgttcccgag ggacgtcttc atgggtccac agtatggata cctcaccctg	1140
aacaacggga gtcaggcggg aggcagctct cctttttact gcctggagta ctttcttct	1200
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc	1260
cacagcagct acgctcacag ccagagtctg gatcggtga tgaatcctct gatcgaccag	1320
tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta	1380
ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg gctgcctgga	1440
ccttgctaca gacagcagcg tctgtcaaa gaggcaaac acaacaaca cagcaacttt	1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga	1560
ccagctatgg ccagtcacaa ggatgacgaa gaaaagtgtt tccccatgca tggaaccctg	1620
atatttggt aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca	1680
gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg gactgtgtca	1740
aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatca ccaaggagcg	1800
ttacctggta tgggtgtggc ggatcgagat gtgtaccttc agggaccat ttgggccaag	1860
attcctcaca ccgatggaca ctttcactct tctccactga tgggaggttt tggactcaaa	1920
caccgcctc ctcagattat gatcaaaaac actcccgttc cagccaatcc tcctacaaac	1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacaataa tggcgtgtac	2160
tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaa	2208

<210> 50  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.15

```

<400> 50
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtggtgga agctcaaac tggcccacca ccaccaaac cgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactctac 180
aaggagagcg cggtcgacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga gggttcttga acctctgggc ttggttgggg agcctgttaa aacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcttc gggaaccgga 480
aaagcgggca accagcctgc aaaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct 600
actacaatgg ctacaggcag tggcgacca gtggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720
accaccagca cccgaacctg ggctctgccc acctacaata accacctcta caagcaaatc 780
tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt cacttgccac ttttcaccac gtgaccggca aagactcatc 900
aacaacaact ggggattccg accaaaaaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggcca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggcttggc gcatcaagga 1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccttg 1140
aacaacggga gtcaggcggg aggacgctct tccttttact gcctggagta ctttcttctt 1200
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgttcctttc 1260
cacagcagct acgctcacag ccagagtctg gatcggtga tgaatcctct gatcgaccag 1320
tacctgtatt atctgaacaa gacacaatca aatagtggaa ctcttcagca gtctcggcta 1380
ctgttttagc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tggaaccttg 1620
atattttgga aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtagcg atatgtgtca 1740
aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctgga tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcctcaca ccgatggaca ctttcatcct tctccactta tgggagggtt tggaactcaa 1920
caccacctc ctcagatcat gattaaaaac actcccgttc cagccaatcc tcccacaaac 1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca agtcagcgtg 2040
gagatcgagt gggagctgca gaaggaggac agcaaacgct ggaaccccga gatccagtac 2100
acttccaact ataacaacc tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 51
<211> 2208
<212> DNA
<213> Unknown

```

```

<220>
<223> new AAV serotype, clone hu.16

```

```

<400> 51
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccgccaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactctac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccg cgcgaggttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga gggttcttga acctctgggc ttggttgagg agcctgttaa aacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
aaagcgggca accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttg tctgggatct 600
actacaatgg ctacaggcag tggcgacca gtggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcca cagagtcac 720
accaccagca cccgaacctg ggctctgccc acctacaaca accacctcta caagcaaatc 780
tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcac 900
aacaacaact ggggattccg accaaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggcca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct 1200
cagatgctgc gtactggaaa caactttcag ttcagctaca ctttgaaga cgttctttc 1260
cacagcagct acgctcacag ccagagtctg gatcggtgga tgaatcctt gatcgaccag 1320
tacctgtatt atctgaacaa gacacaatca aatagtggaa cccttcagca gtctcggtc 1380
ctgttttagc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagc tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagccacaa agacgatgaa gaaaagtfff tccccatgca tggaacctg 1620
atatttggtg aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740
aataatttgc aagactcaaa tactgggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcctcaca ccgatggaca ctttcacctt tctccactta tgggaggttt tggactcaaa 1920
caccacctc ctcagatcat gattaaaaac actcccggtc cagccaatcc tcccacaaac 1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca agtcagcgta 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaacccga gatccagtac 2100
acttccaact ataacaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattggg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 52
<211> 2208
<212> DNA
<213> Unknown

```

```

<220>

```

<223> new AAV serotype, clone hu.18

<400> 52  
atggctgccc atgggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
cagtgttgga agctcaaac tggcccacca ccaccaaac ccgcagagcg gcataaggac 120  
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240  
cggcagctcg aaagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300  
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420  
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480  
aaagcgggcc agcagcctgc gagaaaaaga ttgaattttg gtcagactgg agacgcagac 540  
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttg tctgggatct 600  
actacaatgg cttcaggcag tggcgaccca gtggcagaca ataacgaggg tgccgatgga 660  
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatac 780  
tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840  
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900  
aacaacagct ggggattccg acccaaaaga ctcaacttca agctctttaa cattcaagtc 960  
aaagagggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacggtt 1020  
caagtgttta ccgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
tgcctcccg cgttcccagc agacgtcttt atgggtccac agtatggata cctcaccctg 1140  
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct 1200  
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgttcccttc 1260  
cacagcagct acgctcacag ccagagtctg gatcggctgc tgaatcctct gatcgaccag 1320  
tacctatatt atctgaacaa gacacaatca aatagtggaa ctcttcagca gtctcggcta 1380  
ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440  
ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500  
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560  
ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tggaaccctg 1620  
atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680  
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740  
aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800  
ttacctggtg tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860  
attcctcaca cggacgggca ctttcacctt tctccactaa tgggaggttt tgggctcaaa 1920  
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcctacaaac 1980  
ttcagttctt ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040  
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtat 2100  
acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
tcagagcctc gccccattgg caccagatac ccgactcgta atctgtaa 2208

<210> 53  
<211> 2208  
<212> DNA  
<213> Unknown

<220>  
 <223> new AAV serotype, clone hu.8

<400> 53  
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaacaaga 60  
 cagtgggtgga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac 120  
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
 aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240  
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300  
 caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480  
 aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540  
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tttgggatct 600  
 actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660  
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaata 780  
 tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac ccttggggg 840  
 tattttgact tcaacagatt cacttgccac ttttaccac gtgactggca aagactcatc 900  
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960  
 aaagaggta cgcagaatga cggtagcagc acgattgcc aataacctac cagcacgggt 1020  
 cagggtgtta ctgactcggg gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080  
 tgcctcccgc cgtttccagc ggacgtcttc atgggtccac agtatggata cctcacctg 1140  
 aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct 1200  
 cagatgcttc gtactggaaa caactttcag ttacagctaca cttttgaaga cgttccttc 1260  
 cacagcagct acgctcacag ccagagtctg gatcggtgta tgaatcctt gatcgaccag 1320  
 tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta 1380  
 ctgtttatgc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440  
 ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500  
 ccctggactg cggctacaaa gtaccaccta aatggccggg actcgttggg taatccagga 1560  
 ccagctatgg ccagtcacaa agacgatgaa gaaaagtgtt tccccatgca tggaaacctg 1620  
 atatttggt aacaaggaac aatgctaac gacgcggatt tggacaatgt catgattaca 1680  
 gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740  
 aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800  
 ttacctggca tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860  
 attcctcaca ccgatggaca ctttcatcct tctccactga tgggagggtt tgggctcaaa 1920  
 caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980  
 ttcagtctg ccaagtgtg tcttttcatc acacagtatt ccacggggca ggtcagcgtg 2040  
 gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100  
 acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160  
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 54  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
<223> new AAV serotype, clone rh.56

<400> 54  
atggctgccg atggttatct tccagattgg ctccaggaca ctctctctga aggaataaga 60  
cagtgttgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120  
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
aaggggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240  
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagtgt 300  
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480  
aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540  
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tttgggatct 600  
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660  
gtgggtaatt cttcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
accaccagca cccgaacctg ggcccagccc acctacaaca accacctcta caagcaaatc 780  
tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840  
tattttgact tcaacagatt cactgccac ttttcaccac gtgactggca aagactcac 900  
aacaacaact ggggatttcg acccaagaga ctcaacttca agtcttttaa cattcaagtc 960  
aaagagggtca cgcagaatga cggtagcagc acgattgcc aataacctac cagcacggtt 1020  
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080  
tgcctcccgc cgtttccagc ggacgtcttc atgggtccac agtatggata cctcacctg 1140  
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct 1200  
cagatgcttc gtactggaaa caactttcag ttcagctaca cttttgaaga cgttcctttc 1260  
cacagcagct acgctcacag ccagagtctg gatcggtga tgaatcctct gatcgaccag 1320  
tacctgtatt atctgaacaa aacacaatca aatagtggag ctcttcagca gtctcgcta 1380  
ctgtttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440  
ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500  
ccctggactg cggctacaaa gtaccaccta aatggccggg actcgttggg taatccagga 1560  
ccagctatgg ccagtcacaa agacgatgaa gaaaagtgtt tccccatgca tggaaccctg 1620  
atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680  
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740  
aataatttgc aaaactcaaa tactgggtcca actactggaa ctgtcaatca ccgaggagcg 1800  
ttacctggca tgggtgtgga ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860  
attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920  
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980  
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040  
gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100  
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160  
tcagagcctc gcccatttgg caccagatag ctgactcgta atctgtaa 2208

<210> 55  
<211> 2208  
<212> DNA

<213> Unknown

<220>

<223> new AAV serotype, clone hu.7

<400> 55

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac	120
gacagcaggg gtctttgtgt tcctgggtac aagtacctcg gaccttcaa cggactcgac	180
aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg gacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac	540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttg tttgggatct	600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga	660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcca cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaata	780
tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcac	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagaggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga	1080
tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcacctg	1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct	1200
cagatgttct gtactggaaa caactttcag tttagctaca cctttgaaga cgttcctttc	1260
cacagcagct acgtcacag ccagagtctg gatcggtgga tgaatcctct gatcgaccag	1320
tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta	1380
ctgttttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga	1440
ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt	1500
ccctggactg cggctacaaa gtatcaccta aatggccggg actcgttggt taatccagga	1560
ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg	1620
atattttgga aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca	1680
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca	1740
aataattttg aaaactcaaa tactgggtcca actactggaa ctgtcaatca ccaaggagcg	1800
ttacctggca tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag	1860
attcctcaca ccgatggaca ctttcacctt tctccactga tgggagggtt tgggctcaa	1920
caccgcctc ctcatatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac	1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 56

<211> 2208

<212> DNA  
<213> Unknown

<220>  
<223> new AAV serotype, clone hu.10

<400> 56  
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
cagtgggtgga agctcaaacc tggcccacca ccaccaaacg tcgcagagcg gcatcaggac 120  
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
aaaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240  
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300  
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480  
aaggcggggc atcagcctgc gagaagaga ttgaattttg gtcagactgg agacgcagac 540  
tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tctgggatct 600  
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660  
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctggcgca cagagtcac 720  
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780  
tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840  
tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900  
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960  
aaagaggta cgcagaatga cggtagcagc acgattgccg ataaccttac cagcacggtt 1020  
cagggtgtta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
tgccctccgc cgtttccagc ggacgtcttc acggctccac agtatggata cctcaccctg 1140  
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttctt 1200  
cagatgtctg gtactggaaa caaccttacc ttcagctaca cctttgagga cgttcttctt 1260  
cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctt gatcgaccag 1320  
tatctatat atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380  
ctgttttagc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440  
ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaaca cagcaacttt 1500  
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560  
ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620  
atatattgga aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680  
gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740  
aataatttgc aaaactcaaa tactgggtcca actacagaaa atgtcaatca ccaggagcgc 1800  
ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860  
attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920  
caccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980  
tacagtcttg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040  
gagattgagt gggagctgcg gaaggagaac agcaaacgct ggaaccccg gatccagtat 2100  
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaa 2208

<210> 57

<211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.11

<400> 57  
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
 cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcatcaggac 120  
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
 aaaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240  
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300  
 caggagcgct ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480  
 aaagcgggcc atcagcctgc gagaagaga ttgaattttg gtcagactgg agacgcagac 540  
 tccgtacctg accccagacc tctcggacag ccaccagcag cccccacaag tttgggatct 600  
 actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660  
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780  
 tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840  
 tattttgact tcaacagatt ccactgtcac ttctcccccac gtgattggca aagactcatc 900  
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960  
 aaggagggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt 1020  
 cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
 tgccctccgc cgtttccagc ggacgtcttc atgggtccac agtatggata cctcaccctg 1140  
 aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttctt 1200  
 cagatgctgc gtactggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260  
 cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320  
 tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380  
 ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440  
 ccttgctaca gacagcagcg tctttcaaag caggcaaacy acaacaaca cagcaacttt 1500  
 ccctggactg cggctacaaa gtatcgtcta aatggccggg actcgttggg taatccagga 1560  
 ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tggaaacctg 1620  
 atatttggtg aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680  
 gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740  
 aataatttgc aaaactcaaa tactgggtcca actacagaaa atgtcaatca ccaggggagcg 1800  
 ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacctat ttgggccaag 1860  
 attcctcaca ccgacggaca ctttcacctt tctccactga tgggagggtt tggactcaaa 1920  
 caccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980  
 ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040  
 gagattgagt gggagctgca gaaggagaac agcaaacgct ggaacccgga gatccagtat 2100  
 acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 58  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.9

<400> 58  
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
 cagtgggtga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcatcaggac 120  
 aacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccctccaa cggactcgac 180  
 aaaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240  
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagtgt 300  
 caggagcgct ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcttc gggaaccgga 480  
 aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540  
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccc'cacaag tttgggatct 600  
 actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660  
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780  
 tccagccaat caggagcctc gaacgacaac cactactttg gctgcagcac cccctggggg 840  
 tattttgact tcaacagatt ccactgtcac ttctcccccac gtgattggca aagactcatc 900  
 aacaacaact ggggattccg acccaagaga ctcaacttca agtcttttaa cattcaagtc 960  
 aaagagggtc cgcagaatga cggtagcagc acgattgcc aataacctac cagcacggtt 1020  
 cagggtgttt ctgactcgga gtaccgctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
 tgcctcccgc cgtttccagc ggacgtcttc atgggtccac agtatggata cctcacctg 1140  
 aacaacggga gtcaggcggg aggacgtctc tccttttact gcctggagta ctttcttct 1200  
 cagatgtctg gtaccgga aacttttacc ttcagctaca cttttgagga cgttcctttc 1260  
 cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320  
 tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380  
 ctgttttagc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440  
 ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaaca cagcaacttt 1500  
 cctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560  
 ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tggaaccctg 1620  
 atatttggt aacaaggaac aatgctaac gacgcggatt tggagcatgt tatgattaca 1680  
 gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740  
 aataatttgc aaaactcaaa tactgggtcca actacagaaa atgtcaatca ccaggagcg 1800  
 ttacctggt tgggtgtggc ggatcgagac gtgtacctgc agggaccat ttgggccaag 1860  
 attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920  
 caccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980  
 ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040  
 gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100  
 acttccaact acaacaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
 tcagagcctt gcccatttgg caccagatac ctgactcgta atctgtaa 2208

<210> 59  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.12

```

<400> 59
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga      60
cagtgggtgga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcatcaggac      120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180
aaaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt      300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480
aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac      540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct      600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga      660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac      720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaata      780
tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg      840
tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc      900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc      960
aaagagggtca cgcagaatga cggtagcagc acgattgcc aataaccttac cagcacgggt      1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga      1080
tgcctcccg cgtttccagc ggacgtcttc atgggtccac agtatggata cctcaccctg      1140
aacaacggga gtcaggcggg aggagcgcct tccttttact gcctggagta ctttccttct      1200
cagatgctgc gtactggaaa caactttacc ttcagctaca cctttgagga cgttcctttc      1260
cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag      1320
tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta      1380
ctgttttagc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga      1440
ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaaca cagcaacttt      1500
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga      1560
ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tgggaccctg      1620
atatttggt aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca      1680
gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca      1740
aataatttgc aaaactcaaa tactgggtcca actacagaaa atgtcaatca ccagggagcg      1800
ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag      1860
attcctcaca ccgacggaca ctttcaccct tctccactga tgggagggtt tggactcaaa      1920
caccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac      1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg      2040
gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccg gatccagtat      2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat      2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa      2208

```

<210> 60  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.23

```

<400> 60
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga      60
cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac      120
gacagcaggg gtcttgtgct tccttgggtac aagtacctcg gaccttcaa cggactcgac      180
aaggagagcg cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgggagttt      300
caggagcgct ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga      480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac      540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact      600
aatacgatgg cttcaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga      660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac      720
accaccagca cccgcacctg ggccctgccc acctgcaaca accatctgta caagcaaata      780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg      840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcac      900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc      960
aaagaggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt      1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga      1080
tgcctcccg cgttcccgag agacgtcttc atggtgccac agtatggata cctcaccctg      1140
aacaacggca gtcaggcggg aggacgctct tccttttact gcctggagta ttttccttct      1200
cagatgcttc gtaccggaac caactttacc ttcagctaca cttttgaaga cgttcctttc      1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag      1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccagat gtccaggctt      1380
cagttttctc aggcgggagc aagtgcatt cgggaccagt ctgaaactg gcttcctgga      1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac      1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc      1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc      1620
atctttgga aacaagactc gggaaaaact aatgtggaca ttgaaaagg tatgattaca      1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct      1740
acctacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggt      1800
cttcaggga tggcttgga ggacagagac gtgtacctgc gggggcccat ctgggcaaag      1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt tggacttaaa      1920
caccctctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact      1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacggggca ggtcagcgtg      2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtag      2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat      2160

```

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa

2208

<210> 61  
<211> 2208  
<212> DNA  
<213> Unknown

<220>  
<223> new AAV serotype, clone hu.26

<400> 61  
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
cagtgggtga agctcaaac tggcccacca ccaccaaac ccgcagagcg gcataaggac 120  
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
aaggggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240  
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300  
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
ggaaaaaaga ggccggtaga gcaactctct gcggagccag actcctcctc gggaaccgga 480  
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540  
tcagtacctg accccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600  
aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660  
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720  
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaata 780  
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840  
tattttgact tcaacagatt ccaactgccac ttctccccac gtgactggca aagactcatc 900  
aacaacaact ggggattccg gcccaagaga ctacagcttca agctctttaa cattcaagtc 960  
aaagaggta cgcagaatga cgggtacgac acgattgccca ataaccttac cagcacgggt 1020  
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140  
aacaacggca gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct 1200  
cagatgcttc gtaccgaaa caactttacc ttcagctaca cttttgaaga cgttccttc 1260  
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctt catcgaccag 1320  
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccagat gtccaggctt 1380  
cagttttctc aggccggagc aagtgcatt cgggaccagt ctagaaactg gcttctctgga 1440  
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgattac 1500  
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560  
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620  
atctttgaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tatgattaca 1680  
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740  
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800  
cttcaggga tggcttgga ggacagagac gtgtacctgc aggggcccac ctgggcaaa 1860  
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggactaaa 1920  
cacctcctc cacaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980  
ttcagtgcgg caaagtttgc ttcctcatc acacagtact ccacggggca ggtcagcgtg 2040  
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100  
acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 62  
<211> 2208  
<212> DNA  
<213> Unknown

<220>  
<223> new AAV serotype, clone hu.19

<400> 62  
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
cagtgggtga agctcaaac tggcccacca ccaccaaacg ccgcagagcg gcataaggac 120  
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
aaggagagcg cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240  
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300  
caggagcgct ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480  
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gccagactgg agacgcagac 540  
tcagtacctg accccagacc tctcggacag ccaccagcag cccctcttgg tctgggaact 600  
aatacgatgg cttcaggcag tggcgacca atggcagaca ataacgaggg cgcgcagga 660  
gtgggtaatt cctcgggaaa ttggtattgc gattccacat ggatggcgga cagagtcac 720  
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780  
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840  
tattttgact tcaacagatt cactgccac ttctcccccac gtgactggca aagactcatc 900  
aacaacaact ggggattccg gcccagaga ctacagctta agtcttttaa cattcaagtc 960  
aaagagggtc cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020  
cagggtgttt ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140  
aacaacggca gtcaggcggg aggacgctct tccttttact gcctggagta ctttcttct 1200  
cagatgcttc gtaccggaac caactttacc ttcagctaca cttttgaaga cgttcttct 1260  
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320  
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccagat gtccaggctt 1380  
cagttttctc aggcgggagc aagtgcattc cgggaccagt ctagaaactg gcttcttgg 1440  
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgattac 1500  
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560  
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620  
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg ttatgattaca 1680  
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740  
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800  
cttcaggga tggctcggca ggacagagac gtgtacctgc agggggccat ctgggcaaa 1860  
attccacaca cggacggaca ttttcacccc tctcccctcg tggcggtatt cggacttaa 1920  
caccctcctc cacaatttct catcaagaac accccggtag ctgcgaatcc ttcgaccact 1980  
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacggggca ggtcagcgtg 2040  
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 63  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.20

<400> 63	
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aggtacctcg gaccttcaa cggactcgac	180
aaggagagcg cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga caaccggtac ctcaagtaca accacgtcga cgcggagttt	300
caggagcgctc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa ggcggctccg	420
ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact	600
aatacgatgg cttcaggcag tggcgacca atggcagaca ataacgaggg cgcgcagga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaacc	780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg	840
cattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc	900
aacaacaact ggggattccg gcccaagaga ctacagctca agctctttaa cattcaagtc	960
aaagaggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccg cgttccagc agacgtcttc atggtgccac agtatggata cctcaccctg	1140
aacaacggca gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct	1200
cagatgcttc gtaccgaaa caactttacc ttcagctaca ctttgaaga cgttcctttc	1260
catagcagct acgtcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccagat gtccaggctt	1380
cagttttctc aggcgggagc aagtgcatt cgggaccagt ctagaaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgattac	1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc	1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc	1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tatgattaca	1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt	1800
cttcaggga tggcttgga ggacagagac gtgtacctgc aggggcccat ctgggcaaag	1860
attccacaca cggacggaca ttttcacccc tctccccca tgggcggatt cggacttaa	1920
cacctcctc caaaaattct catcaagaac accccgggtac ctgcgaatcc ttcgaccact	1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacggggca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtag	2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
tcagagcctc gccccattgg cgccagatac ctgactcgta atctgtaa 2208

<210> 64  
<211> 2208  
<212> DNA  
<213> Unknown

<220>  
<223> new AAV serotype, clone hu.27

<400> 64  
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
cagtgggtga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120  
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240  
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcgaggttt 300  
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480  
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540  
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggaact 600  
aatacgatgg cttcaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga 660  
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720  
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaact 780  
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840  
tatttcgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900  
aacaacaact ggggattccg gcccaagaga ctacagctca agctctttaa cattcaagtc 960  
aaagagggtc cgcagaatga cggtagcagc acgattgccg ataaccttac cagcacggtt 1020  
caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
tgccttccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140  
aacaacggca gtcaggcggg aggacgctct tccttttact gcctggagta ctttccttct 1200  
cagatgcttc gtaccggaag caactttacc ttcagctaca cctttgaaga cgttcctttc 1260  
catagcagct acgctcacgg ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320  
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgat gtccaggctt 1380  
cagttttctc aggcgggagc aagtgcggtt cgggaccagt ctgaaaactg gcttcctgga 1440  
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgtattac 1500  
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560  
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cgggggttctc 1620  
gtccttgga aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgattaca 1680  
gacgaagagg aaatcaggac caccaatccc gcggctacgg agcagtatgg ttctgtatct 1740  
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggtt 1800  
cttccaggca tggcttgga ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860  
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920  
caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980  
ttcagtgcgg caaagtttgt ttccttcac acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 65  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.21

<400> 65	
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtctttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagcg cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac	240
cggcagctcg acagcggaga taaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaagaga ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg acccccggcc tctcggacag ccaccagcag cccctctggt tctgggaact	600
aatacgtatg cttcaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatac	780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg	840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc	900
aacaacaact ggggattccg gcccagaga ctacagcttca agctctttaa cattcaagtc	960
aaagagggtca cgcagaatga cggtagcagc acgattgccg ataacttac cagcacgggt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgctctccgc cgttccagc agacgtcttc atggtgccac agtatggata cctcacctg	1140
aacaacggca gtcaggcggg aggcagctct tccttttact gcctggagta ctttcttct	1200
cagatgcttc gtaccggaac caactttacc ttcagctaca cttttgaaga cgttccttc	1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgat gtccaggctt	1380
cagttttctc aggcgggagc aagtgcatt cgggaccagt ctgaaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgattac	1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc	1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc	1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgattaca	1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggt	1800
cttccaggca tggctcggca ggacagagac gtgtacctgc agggggccat ctgggcaaaag	1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa	1920
cacctcctc cacaattct catcaagaac acccgggtac ctgcgaatcc ttcgaccact	1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacggggca ggtcagcgtg	2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 66  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.24

<400> 66	
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggagagcg cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga taacctgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg acccccggcc tctcggacag ccaccagcag cccctcttgg tctgggaact	600
aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgcgcagcga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaact	780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg	840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc	900
aacaacaact ggggatttcg gcccaagaga ctcagcttca agtcttttaa cattcaagtc	960
aaagaggta cgcagaatga cggtagcagc acgattgcc aataaccttac cagcacgggt	1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg	1140
aacaacggca gtcaggcggg aggcagctct tccttttact gcctggagta ctttcttct	1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttctttc	1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgat gtccaggctt	1380
cagttttctc aggcgggagc aagtgcatt cgggaccagt ctgaaaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgattac	1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc	1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cgggggttctc	1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg ttagattaca	1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt	1800
cttcagggca tggctctggc ggacagagac gtgtacctgc agggggccat ctgggcaaag	1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaa	1920
cacctcctc cacaaattct catcaagaac accccggtag ctgcgaatcc ttcgaccact	1980

ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacggggca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaaatc tggttaatgtg gactttactg tggacactaa tgggtgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 67  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.22

<400> 67	
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aaggggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact	600
aatacgatgg cttcaggcag tggcgacca atggcagaca ataacgaggg cgcgcagcga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcgg cagagtcac	720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc	780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg	840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc	900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc	960
aaagagggtca cgcagaatga cggtagcagc acgattgcc aataaccttac cagcacgggt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg	1140
aacaacggca gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct	1200
cagacgcttc gtaccggaac caactttacc ttcagctaca cctttgaaga cgttcctttc	1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgat gtccaggctt	1380
cagttttctc aggcgggagc aagtgcattc cgggaccagt ctagaaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac	1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc	1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc	1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tatgattaca	1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt	1800
cttccaggca tggctctggc ggacagagac gtgtacctgc agggggccat ctgggcaaag	1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa	1920
caccctcctc cacaaattct catcaagaac accccggtag ctgcgaatcc ttcgaccact	1980

ttcagtcg	caaagtttgc	ttccttcac	acacagtact	ccacggggca	ggtcagcgtg	2040
gagatc	gagtcgca	gaaggagaac	agcaaacgct	ggaatcccga	aattcagtac	2100
acttccaact	acaacaaatc	tgttaatgtg	gactttactg	tggacactaa	tgggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 68  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.28

<400> 68		
atggctgccc	atggttatct tccagattgg	ctcgaggaca ctctctctga aggaataaga 60
cagtggtgga	aactcaaacc tggcccacca	ccaccaaacg cgcagagcg gcataaggac 120
gacagcaggg	gtcttgtgct tcctgggtac	aagtacctcg gaccttcaa cggactcgac 180
aagggagagc	cggtaacga ggcagacgcc	gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg	acagcggaga caaccctgac	ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc	ttaaagaaga tacgtctttt	gggggcaacc tcggacgagc agtcttccag 360
gcaaaaaaga	gggttctgga acctctgagc	ctggttgagg agcctgttaa gacggctccg 420
ggaaaaaaga	ggccggtaga gcactctccc	gcagagccag attcctcctc cggaactgga 480
aagtcgggca	accagcctgc aagaaagaga	ttgaatttcg gtcagactgg agactcagac 540
tccgtacctg	acccccagcc tctcggacag	ccaccagcag cccctcttgg tctgggaact 600
aatacgaagg	ctacaggcag tggcgcacca	atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt	cctcgggaaa ttggcattgc	gattccacat ggatgggcca cagagtcac 720
accaccagca	cccgaacctg ggccctgccc	acctacaaca accatctgta caagcaaata 780
tccagccagt	ctggagccag caacgacaat	cactactttg gctacagcac cccctggggg 840
tattttgact	tcaacagatt ccactgccac	ttttcaccac gtgactggca aagactcac 900
aacaacaact	ggggatttcg acccaagaga	ctcaacttca agctctttaa cattcaagtc 960
aaagaggtca	cgcagaatga cggtagcagc	acgattgcca ataaccttac cagcacggtt 1020
caggtgttta	ctgactcgga gtaccagctc	ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccgc	cgttcccagc agacgtcttc	atgggtgccac agtatggata cctcaccctg 1140
aacaacggga	gtcaggcagc aggacgtctt	tcattttact gcctagagta ctttccttct 1200
cagatgctgc	gtaccggaaa caactttacc	ttcagctaca cctttgagga cgttcctttc 1260
cacagcagct	acgtcacag ccagagtttg	gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt	acttgagcag aacaaacact	ccaagcggaa ccaccagca gtccaggctt 1380
cagttttctc	aggccggagc gagtgacatt	caggaccagt ctaggaaactg gcttcctgga 1440
ccctgttacc	gtcagcagcg agtatcaaag	acatctgcgg ataacaacaa cagtgaatac 1500
tcgtggactg	gagctaccaa gtaccacctc	aatggcagag actctctggt gaatccgggc 1560
ccggccatgg	ccagccacaa agacgatgaa	gaaaagtttt ttcctcagag cggggttctt 1620
atctttggga	agcaaggctc agagaaaaca	aatgtggata ttgaaaaggc catgattaca 1680
gacgaagagg	aaatcaggac caccaatccc	gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc	agagcggcaa cacacaagca	gctaccgcag atgtcaacac acaaggcgtt 1800
cttcaggga	tggtcgggca agacagagac	gtgtacctgc aggggcctac ttgggcaaaag 1860
attccacaca	cggacggaca ttttcacccc	tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc	cacagattct	catcaagaac	accccggtag	ctgcgaatcc	ttcgaccacc	1980
ttcagtgagg	caaagtttgc	ttccttcatt	acacagtact	ccacggggca	ggtcagcggtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	gatccagtac	2100
acttccaact	acaacaagtc	tgtaaatgtg	gactttactg	tggacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 69  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.29

<400> 69		
atggctgccc	atggttatct	60
cagtgggtga	agctcaaacc	120
gacagcaggg	gtcttgtgct	180
aagggagagc	cgggtcaacga	240
cggcagctcg	acagcggaga	300
caggagcgcc	ttaaagaaga	360
gcaaaaaaga	gggttctgga	420
ggaaaaaaga	ggccggtaga	480
aagtcgggca	accagcctgc	540
tccgtacctg	acccccagcc	600
aatacgatgg	ctacaggcag	660
gtgggtaatt	cctcgggaaa	720
accaccagca	cccgaacctg	780
tccagccagt	ctggagccag	840
tattttgact	tcaacagatt	900
aacaacaact	ggggattccg	960
aaagagggtc	cgcagaatga	1020
cagggtgtta	ctgactcgga	1080
tgccctccgc	cgttcccagc	1140
aacaacggga	gtcaggcagt	1200
cagatgctgc	gtaccggaaa	1260
cacagcagct	acgctcacag	1320
tacctgtatt	acttgagcag	1380
cagttttctc	agggcggagc	1440
ccctgttacc	gtcagcagcg	1500
tcgtggactg	gagctaccaa	1560
ccggccatgg	ccagccacaa	1620
atctttggga	agcaaggccc	1680
gacgaagagg	aaatcaggac	1740
accaacctcc	agagcggcaa	1800
cttcaggga	tggctctggca	1860
attccacaca	cggacggaca	1920

caccctctc	cacagattct	catcaagaac	accccgttac	ctgcgaatcc	ttcgaccacc	1980
ttcagtgcg	caaagtttgc	ttccttcatt	acacagtact	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	gatccagtac	2100
acttccaact	acaacaagtc	tgtaaatgtg	gactttactg	tggacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 70  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.30

<400> 70	
atggctgccg	atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga	agctcaaac tggcccacca ccaccaaacg ccgcagagcg gcataaggac 120
gacagcaggg	gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc	cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg	acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc	ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcaaaaaaga	gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg 420
ggaaaaaaga	ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480
aagtcgggca	accagcctgc aagaagaga ttgaatttcg gtcagactgg agactcagac 540
tccgtacctg	acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatacgatgg	ctacaggcag tggcgacca atggcagaca ataacgaggg cgcgcagga 660
gtgggtaatt	cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca	cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780
tccagccagt	ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840
tattttgact	tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc 900
aacaacaact	ggggattccg acccaagaga ctcaacttca agtcttttaa cattcaagtc 960
aaagagggtca	cgcagaatga cggtagcagc acgattgccca ataactttac cagcacgggt 1020
cagggtgttta	ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg	cgttccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga	gtcaggcagt aggacgtctc tcattttact gcctagagta ctttccttct 1200
cagatgctgc	gtaccggaata cagctttacc ttcagctaca cctttgagga cgttcctttc 1260
cacagcagct	acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt	acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380
cagttttctc	aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440
ccctgttacc	gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500
tcgtggactg	gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg	ccagccacaa agacgatgaa gaaaagtctt ttcctcagag cggggttctt 1620
atctttggga	agcaaggctc agagaaaaca aatgtggata ttgaaaagg catgattaca 1680
gacgaagagg	aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc	agagcggcaa cacacaagca gctaccgag atgtcaacac acaaggcgtt 1800
cttcaggga	tggctctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa	1920
cacctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc	1980
ttcagtgctg caaagtttgc ttccttcatt acacagtact ccacggggca ggctagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac	2100
acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 71  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.13

<400> 71	
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaac tggcccacca ccaccaaac cgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac	180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag	360
gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac	540
tccgtacctg accccagcc tctcgacag ccaccagcag cccctctgg tctgggaact	600
aatacgatgg cttcaggcag tggcgacca atggcagaca ataacgagg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgaacttg ggccctgccc acctacaaca accatctcta caagcaaata	780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt cacttgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggatttcg gcccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagaggta cgcagaatga cggtagcag acgattgcca ataaccttac cagcacggtt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccg cgttccagc agacgtcttc atggtgccac agtatggata cctcaccctg	1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttccttct	1200
cagatgctgc gtaccggaac caactttacc ttcagctaca cctttgagga cgttcctttc	1260
cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgca gtccaggctt	1380
cagttttctc aggcgggagc aagtgacatt cgggaccagt ctaggaaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca	1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctgc agggcggcaa cacacaagca gctaccgag atgtcaacac acaaggcgtt	1800
cttccaggca tggctctggca ggacagagac gtgtacctgc aggggcccac ctgggcaaag	1860

attccacaca	cggacggaca	ttttcacccc	tctcccctca	tgggcggatt	cggacttaaa	1920
cacctcctc	cacagattct	catcaagaac	accccgttac	ctgcgaatcc	ttcgaccacc	1980
ttcagtgcg	caaagtttgc	ttctttcatc	acacagtatt	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	gatccagtac	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	ttgacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 72  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.34

<400> 72		
atggctgccc	atggttatct	tccagattgg
cagcgggtgga	agctcaaacc	tggcccacca
gacagcaggg	gtctttgtgt	tccttgggtac
aaggagagagc	cgggtcaacga	ggcagacgcc
cggcagctcg	acagcggaga	caacccgtac
caggagcgcc	ttaaagaaga	tacgtccttt
gcgaaaaaga	gggtacttga	acctctgggc
ggaaaaaaga	ggccggtaga	gcactctcct
aaggcggggc	agcagcctgc	aagaaaaaga
tcagtacctg	acccccagcc	tctcggacag
aatacgatgg	ctacaggcag	tggcgcacca
gtgggtaatt	cctcgggaaa	ttggcattgc
accaccagca	cccgaacctg	ggccctgccc
tccagccaat	caggagcctc	gaacgacaat
tattttgact	tcaacagatt	ccactgccac
aacaacaact	ggggatttccg	acccaagaga
aaagagggtca	cgcagaatga	cggtagcagc
cagggtgttta	ctgactcgga	gtaccagctc
tgccctccgc	cgttcccagc	agacgtcttc
aacaacgaga	gtcaggcagt	aggacgtctc
cagatgctgc	gtaccggaaa	caactttacc
cacagcagct	acgctcacag	ccagagtctg
tacctgtatt	acttgagcag	aacaaacact
cagttttctc	aggccggagc	gagtgacatt
ccctgttacc	gccagcagcg	agtatcaaag
tcgtggactg	gagctaccaa	gtaccacctc
ccggccatgg	caagccacaa	ggacgatgaa
atctttggga	agcaaggctc	agagaaaaca
gacgaagagg	aaatcaggac	aaccaatccc
accaacctcc	agagaggcaa	cagacaagca
		gctaccgcag
		atgtcaacac
		acaaggcgtt

cttccaggca tgggtctggca ggacagagat gtgtaccttc agggggcccat ctggggcaaag	1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa	1920
caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc	1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacgggaca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccg aattcagtac	2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 73  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.35

<400> 73	
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagcggtgga agctcaaac tggcccacca ccaccagagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggacttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gactctcct gtggagccag actcctcctc gggaaccgga	480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttg tctgggaact	600
aatacgtagg ctacaggcag tggcgacca atggcagaca ataacgagg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggca cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt	780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagaggta cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcttcccgc cgttcccagc agacgtcttc atggtaccac agtatggata cctcaccctg	1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttccttct	1200
cagatgctgc gtaccggaac caactttacc ttcagctaca cttttgagga cgttcctttc	1260
cacagcagct acgtcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaacact ccaagtggaa ccaccagca gtcaaggctt	1380
cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga	1440
ccctgttacc gccagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagtaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca	1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt	1800

cttccaggca	tggtctggca	ggacagagat	gtgtaccttc	aggggcccac	ctgggcaaag	1860
attccacaca	cggacggaca	ttttcacccc	tctccctca	tgggtggatt	cggacttaaa	1920
cacctctctc	cacagattct	catcaagaac	accccggtag	ctgcgaatcc	ttcgaccacc	1980
ttcagtgctg	caaagtttgc	ttccttcctc	acacagtact	ccacgggaca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	aattcagtac	2100
acttccaact	acaacaagtc	tgtaaatgtg	gactttactg	tggacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 74  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.36

<400>	74	
atggctgccc	atggttatct	tccagattgg
	ctcagaggaca	ctctctctga
	aggaataaga	60
cagcgggtga	agctcaaac	tggccacca
	ccaccagagc	ccgcagagcg
	gcataaggac	120
gacagcaggg	gtcttgtgct	tcctgggtac
	aagtacctcg	gaccttcaa
	cggactcgac	180
aaggagagc	cggtaacga	ggcagacgcc
	gcggccctcg	agcacgacaa
	agcctacgac	240
cggcagctcg	acagcggaga	caaccgtac
	ctcaagtaca	accacgccga
	cgcggagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt
	gggggcaacc	tcggacgagc
	agtcttccag	360
gcgaaaaaga	gggtactcga	acctctgggc
	ctggttgagg	aacctgttaa
	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct
	gtggagccag	actcctcctc
	gggaaccgga	480
aaggcgggccc	agcagcctgc	aagaaaaaga
	ttgaattttg	gtcagactgg
	agacgcagac	540
tcagtacctg	acccccagcc	tctcggacag
	ccaccagcag	ccccctctgg
	tctgggaact	600
aatacgaatg	ctacaggcag	tggcgcacca
	atggcagaca	ataacgaggg
	cgccgacgga	660
gtgggttaatt	cctcgggaaa	ttggcattgc
	gattccacat	ggatgggcga
	cagagtcac	720
accaccagca	cccgaacctg	ggccctgccc
	acctacaaca	accacctcta
	caaacaaatt	780
tccagccaat	caggagcctc	gaacgacaat
	cactactttg	gctacagcac
	cccttggggg	840
tattttgact	tcaacagatt	ccactgccac
	ttttcaccac	gtgactggca
	aagactcatc	900
aacaacaact	ggggattccg	acccaagaga
	ctcaacttca	agctctttta
	cattcaagtc	960
aaagaggtca	cgcagaatga	cggtagcagc
	acgattgcc	ataaccttac
	cagcacgggt	1020
cagggtgttta	ctgactcgga	gtaccagctc
	ccgtacgtcc	tcggctcggc
	gcatcaagga	1080
tgccctccgc	cgttcccgag	agacgtcttc
	atgggtgccac	agtatggata
	cctcacctcg	1140
aacaacggga	gtcaggcagc	aggacgtctc
	tcattttact	gcctggagta
	ctttccttct	1200
cagatgctgc	gtaccggaaa	caactttacc
	ttcagctaca	cttttgagga
	cgttcctttc	1260
cacagcagct	acgtcacag	ccagagtctg
	ggccgtctca	tgaatcctct
	catcgaccag	1320
tacctgtatt	acttgagcag	aacaacact
	ccaagtggaa	ccaccacgca
	gtcaaggctt	1380
cagttttctc	aggccggagc	gagtgacatt
	cgggaccagt	ctaggaactg
	gcttcctgga	1440
ccctgttacc	gccagcagcg	agtatcaaag
	acatctgcgg	ataacaacaa
	cagtgaatac	1500
tcgtggactg	gagctaccaa	gtaccacctc
	aatggcagag	actctctggt
	gaatccgggc	1560
ccggccatgg	caagccacaa	ggacgatgaa
	gaaaagtttt	ttcctcagag
	cggggttctc	1620
atctttggga	agcaaggctc	agagaaaaca
	aatgtggaca	ttgaaaagg
	catgattaca	1680
gacgaagagg	aaatcaggac	aaccaatccc
	gtggctacgg	agcagtatgg
	ttctgtatct	1740

accaacctcc	agagaggcaa	cagacaagca	gctaccgcag	atgtcaacac	acaaggcggt	1800
cttccaggca	tgggtctggca	ggacagagat	gtgtaccttc	aggggcccac	ctgggcaaag	1860
attccacaca	cggacggaca	ttttcacccc	tctcccctca	tgggtggatt	cggacttaaa	1920
cacctcctc	cacagattct	catcaagaac	accccggtag	ctgcgaatcc	ttcgaccacc	1980
ttcagtgctg	caaagtttgc	ttccttcctc	acacagtact	ccacgggaca	ggtcagcggt	2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	aattcagtag	2100
acttccaact	acaacaagtc	cgtaaatgtg	gactttactg	tggacactaa	tggcggtgat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 75  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.33

<400>	75	
atggctgccc	atggttatct	tccagattgg
cagcgggtgga	agctcaaacc	tggcccacca
gacagcaggg	gtcttgtgct	tcctgggtac
aaggggagagc	cggtaacga	ggcagacgcc
cggcagctcg	acagcggaga	caaccctgac
caggagcgcc	ttaaagaaga	tacgtctttt
gcgaaaaaga	gggtacttga	acctctgggc
ggaaaaaaga	ggccggtaga	gcactctcct
aaggcggggc	agcagcctgc	aagaaaaaga
tcagtacctg	acccccagcc	tctcggacag
aatacagatg	ctacaggcag	tggcgacca
gtgggtaatt	cctcgggaaa	ttggcattgc
accaccagca	cccgaacctg	ggccctgccc
tccagccaat	caggagcctc	gaacgacaat
tattttgact	tcaacagatt	ccactgccac
aacaacaact	ggggattccg	acccaagaga
aaagaggatc	cgcagaatga	cggtagcagc
cagggtgttta	ctgactcgga	gtaccagctc
tgcctcccg	cggtccagc	agacgtcttc
aacaacggga	gtcaggcagt	aggacgtctt
cagatgctgc	gtaccggaaa	caactttacc
cacagcagct	acgtctcacag	ccagagtctg
tacctgtatt	acttgagcag	aacaacact
cagttttctc	aggccggagc	gagtgacatt
ccctgttacc	gccagcagcg	agtatcaaag
tcgtggactg	gagctaccaa	gtaccacctc
ccggccatgg	caagccacaa	ggacgatgaa
atctttggga	agcaaggctc	agagaaaaca
gacgaagagg	aaatcaggac	aaccaatccc

accaacctcc	agagaggcaa	cagacaagca	gctaccgcag	atgtcaacac	acaaggcggt	1800
cttccaggca	tggctctggca	ggacagagat	gtgtaccttc	aggggcccac	ctgggcaaag	1860
attccacaca	cggacggaca	ttttcacccc	tctcccctca	tgggtggatt	cggacttaaa	1920
caccttcctc	cacagattct	catcaagaac	accccggtag	ctgcgaatcc	ttcgaccacc	1980
ttcagtgctg	caaagtttgc	ttccttcctc	acacagtact	ccacgggaca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	aattcagtag	2100
acttccaact	acaacaagtc	tggttaagtg	gactttactg	tggacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatag	ctgactcgta	atctgtaa		2208

<210> 76  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.45

<400>	76	
atggctgccc	atggctatct	tccagattgg
cagtgggtgga	agctcaaacc	tggcccacca
gacagcaggg	gtcttctgct	tcctgggtac
aagggagagc	cggtaacga	ggcagacgcc
cggcagctcg	acagcggaga	caaccgtag
caggagcgcc	ttaaagaaga	tacgtctttt
gcgaaaaaga	gggttcttga	acctctgggc
ggaaaaaaga	ggccggtaga	gcactctcct
aaggcggggc	agcagcctgc	aagaaaaaga
tcagtacctg	acccccagcc	tctcggacag
aatacgatgg	ctacaggcag	tggcgcacca
gtgggtaatt	cctcgggaaa	ttggcattgc
accaccagca	cccgaacctg	ggccctgccc
tccagccaat	caggagcctc	gaacgacaat
tattttgact	tcaacagatt	ccactgccac
aacaacaact	ggggattccg	acccaagaga
aaagaggtca	cgcagaatga	cggtagcagc
cagggtgttta	ctgactcggg	gtaccagctc
tgcctcccgc	cgttcccagc	agacgtcttc
aacaacggga	gtcaggcagc	aggacgtctc
cagatgctgc	gtaccggaaa	caactttacc
cacagcagct	acgtcacag	ccagagtctg
tacctgtatt	acttgagcac	aacaacact
cagttttctc	aggccggagc	gagtgacatt
ccctgttacc	gccagcagc	agtatcaaag
tcgtggactg	gagctaccaa	gtaccacctc
ccggccgtgg	caagccacaa	ggacgatgaa
atctttggga	agcaaggctc	agagaaaaca

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaaccttc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcggt	1800
cttcaggga tggctctggca ggacagagat gtgtaccttc agggggcccat ctggggcaaag	1860
attccacaca cggacggaca ttttcacccc tctccctca tgggtggatt cggacttaaa	1920
cacctctctc cacagattct catcaagaac accccggtag ctgcgaatcc ttcgaccacc	1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacgggaca ggtagcggtg	2040
gagatcgagt gggagctgca gaaggaaaac agcaaagcgt ggaatcccga aattcagtac	2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 77  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.47

<400> 77	
atggctgccg atggctatct tccagattgg ctgcaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaagc ccgcagagcg gcatagggac	120
gacagcaggg gtcttctgct tcctgggtac aagtacctcg gaccttcaa cggactcgac	180
aaggagagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca agcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctctt gtggagccag actcctcttc gggaaccgga	480
aaggcggggc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggaact	600
aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgagg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt	780
tccagccaat caggagctc gaacgacagt cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagagggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt	1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcttcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg	1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttcttct	1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttctttc	1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcac aacaacact ccaagtggaa ccaccacgca gtcaaggctc	1380
cagttttctc aggcgggagc gagtgacatt cgggaccagt ctaggaaactg gcttctctga	1440
ccctgttacc gccagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca	1680

gacgaagagg	aaatcaggac	aaccaatccc	gtggctacgg	agcagtatgg	ttctgtatct	1740
accaacctcc	agagaggcaa	cagacaagca	gctaccgcag	atgtcaacac	acaaggcggt	1800
cttcaggga	tggctctggca	ggacagagat	gtgtaccttc	agggggcccat	ctgggcaaag	1860
attccacaca	cggacggaca	ttttcacccc	tctccccctca	tgggtggatt	cggacttaaa	1920
cacctcctc	cacagattct	catcaagaac	accccggtag	ctgcgaatcc	ttcgaccacc	1980
ttcagtgcgg	caaagtctgc	ttccttcctc	acacagtact	ccacgggaca	ggtcagcggt	2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccg	aattcagtag	2100
acttccaact	acaacaagtc	tgtaaatgtg	gactttactg	tggacactaa	tggcggttat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 78  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.48

<400> 78						
atggctgccc	atggttatct	tccagattgg	ctcaggagca	acctctctga	gggcattcgc	60
gagtggtggg	acttgaaacc	tggagccccg	aagcccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gaccttcaaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgcgca	cgccgagttt	300
caggagcgct	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggagcgc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggt	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaac	gtccggtaga	gcagtcgcca	caagagccag	actcctcctc	gggcatcggc	480
aagacaggcc	agcagcccgc	taaaaagaga	ctcaattttg	gccagactgg	cgactcagag	540
tcagtccccg	atccacaacc	tctcggagaa	cctccagcaa	cccccgctgc	tgtgggacct	600
actacaatgg	cttcaggcgg	tggcgaccca	atggcagaca	ataacgaagg	cgccgacgga	660
gtgggtaatg	cctcaggaaa	ttggcattgc	gattccacat	ggctgggcga	cagagtcctc	720
accaccagca	cccgccacctg	ggccttgccc	acctacaata	accacctcta	caagcaaatc	780
tccagtactt	caacgggggc	cagcaacgac	aaccactact	tcggctacgg	caccccttgg	840
gggtattttg	atttcaacag	attccactgc	cacttttcac	cacgtgactg	gcagcgactc	900
atcaacaaca	attgggggatt	ccggcccaag	agactcaact	tcaaactctt	caacatccaa	960
gtcgaaggagg	tcacgacgaa	tgatggcgct	acaaccatcg	ctaataacct	taccagcacg	1020
gttcaagtct	tctcggactc	ggagtaccag	cttcctgtag	tcctcggctc	tgcgcaccag	1080
ggctgcctcc	ctccgttccc	ggcggacgtg	ttcatgattc	cgcaatacgg	ctacctgacg	1140
ctcaacaatg	gcagccaagc	cgtgggacgt	tcattccttt	actgcctgga	atatttcctt	1200
tctcagatgc	tgagaacggg	caacaacttt	accttcagct	acacctttga	ggaagtgcct	1260
ttccacagca	gctacgcgca	cagccagagc	ctggaccggc	tgatgaatcc	tctcatcgac	1320
caatacctgt	attacctgaa	cagaacacaa	aatcagttcc	gaagtggcca	aaacaaggac	1380
ttgctgttta	gccgtgggtc	tccagctggc	atgtctgttc	agcccaaaaa	ctggctacct	1440
ggaccctgtt	atcggcagca	gcgcgtttct	aaaacaaaaa	cagacaacaa	caacagcaat	1500
tttacctgga	ctgggtcttc	aaaatataac	ctcaatgggc	gtgaatccat	catcaaccct	1560
ggcaccgctg	tggcctcaca	caaagacgac	gaagacaagt	tctttcccat	gagcgggtgc	1620

atgatttttg gaaaagagag cgccggagct tcaagcactg cattggacaa tgtcatgatt	1680
acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg	1740
gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga	1800
gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc	1860
aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcg	1920
aagaaccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg	1980
gagttttcag ctacaaagt tgccttattc atcacccaat actccacagg acaagtgagt	2040
gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag	2100
tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt	2160
tatactgagc ctcgccccat tggcaccgt taccttacc gtcccctgta a	2211

<210> 79  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone rh.71

<400> 79	
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtgggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctgggtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc	480
aagacaggcc agcagccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag	540
tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgtgc tgtgggacct	600
actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga	660
gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcac	720
accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaata	780
tccagtgcct caacgggggc cagcaacgac aaccactact tcggctacag caccctctgg	840
gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc	900
atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa	960
gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg	1020
gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag	1080
ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg	1140
ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttcctt	1200
tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct	1260
ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac	1320
caatacctgt attacctgaa cagaactcaa aatcagtcct gaagtgccca aaacaaggac	1380
ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct	1440
ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat	1500
tttacctgga ctggtgcttc aaaatataac ctcaatggc gtgaatccat catcaaccct	1560
ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgc	1620

atgatttttg	gaaaagagag	cgccggagct	tcaaacactg	cattggacaa	tgtcatgatt	1680
acagacgaag	aggaaattaa	agccactaac	cctgtggcca	ccgaaagatt	tgggaccgtg	1740
gcagtcaatt	tccagagcag	cagcacagac	cctgcgaccg	gagatgtgca	tgctatggga	1800
gcattacctg	gcatggtgtg	gcaagataga	gacgtgtacc	tgagggtcc	catttgggcc	1860
aaaattcctc	acacagatgg	acactttcac	ccgtctcctc	ttatgggcgg	ctttggactc	1920
aagaacccgc	ctcctcagat	cctcatcaaa	aacacgcctg	ttcctgcgaa	tcctccggcg	1980
gagttttcag	ctacaaagtt	tgcttcattc	atcacccaat	actccacagg	acaagtgagt	2040
gtggaaattg	aatgggagct	gcagaaagaa	aacagcaagc	gctggaatcc	cgaagtgcag	2100
tacacatcca	attatgcaaa	atctgccaac	gttgatttta	ctgtggacaa	caatggactt	2160
tatactgagc	ctcgcccat	tggcaccgt	taccttacc	gtcccctgta	a	2211

<210> 80  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.43

<400>	80	
atggctgctg	acggttatct	tccagattgg
gagtgggtggg	acctgaaacc	tggagcccc
gacggccggg	gtctggtgct	tcctggctac
aagggggagc	ccgtcaacgc	ggcggacgca
cagcagctca	aagcgggtga	caatccgtac
caggagcgtc	tgcaagaaga	tacgcctttt
gccaagaagc	gggttctcga	acctctcggg
ggaaagaaga	gaccggtaga	accgtcacct
ggcaagaag	gccagcagcc	cgtaaaaag
gagtcagtc	ccgaccctca	accaatcgga
tctgtgtacaa	tggctgcagg	cggtggcgct
ggagtgggta	atgcctcagg	aaattggcat
atcaccacca	gcaccgcac	ctgggccttg
atctccagtg	cttcaacggg	ggccagcaac
tgggggtatt	ttgatttcaa	cagattccac
ctcatcaaca	acaattgggg	attccggccc
caagtcaagg	aggtcacgac	gaatgatggc
acggttcaag	tcttctcgga	ctcggagtag
cagggctgcc	tccctccgtt	cccggcgga
acgctcaaca	atggcagcca	agccgtggga
ccttctcaga	tgctgagaac	gggcaacaac
cctctccaca	gcagctacgc	gcacagccag
gtccaatacc	tgtattacct	gaacagaact
gacttgctgt	tcagccgtgg	gtctccagct
cctggaccct	gttatcgga	gcagcggtt
aattttacct	ggactgggtg	ttcaaaatat

cctggcactg	ctatggcctc	acacaaagac	gacgaagaca	agttctttcc	catgagcgg	1620
gtcatgattt	ttggaaaaga	gagcgccgga	gcttcaaaca	ctgcattgga	caatgtcatg	1680
attacagacg	aagaggaaat	taaagccact	aaccctgtgg	ccaccgaaag	atttgggacc	1740
gtggcagtca	atttccagag	cagcagcaca	gaccctgcga	ccggagatgt	gcatgctatg	1800
ggagcattac	ctggcatggt	gtggcaagat	agagacgtgt	acctgcaggg	tcccatttgg	1860
gccaaaattc	ctcacacaga	tggacacttt	caccctgtct	ctcttatggg	cggcttttga	1920
ctcaagaacc	cgcctcctca	gatcctcatc	aaaaacacgc	ctgttcctgc	gaatcctccg	1980
gctggagttt	cagctacaaa	gtttgcttca	ttcatcacc	aatactccac	aggacaagt	2040
agtgtggaaa	ttgaatggga	gctgcagaaa	gaaaacagca	agcgtggaa	tcccgaagt	2100
cagtacacat	ccaattatgc	aaaatctgcc	agcgttgatt	ttactgtgga	caacaatgga	2160
ctttatactg	agcctcgccc	cattggcacc	cgttacctta	cccgtccct	gtaa	2214

<210> 81  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.44

<400> 81	
atggctgccc	atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga	agctcagacc tggcccacca ccaccaagc ccgcagagcg gcataaggac 120
gacagcaggg	gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aaggagagc	cggtaacga ggcagacgcc gcggccctcg agcacgaca agcctacgac 240
cggcagctcg	acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc	ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag 360
gccaagaagc	gggttctcga acctctcggt ctgggtgagg aaggcgtga gacggctcct 420
ggaaagaaac	gtccggtaga gcagtcgcca caaggccag actcctcctc gggcatcggc 480
aagacaggcc	agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg	atccacaacc tctcggagaa cctccagcaa ccccgctgc tgtgggacct 600
actacaatgg	cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
gtgggtaatg	cctcaggaaa ttggcattgc gattccacat ggctgggcca cagagtcac 720
accaccagca	cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780
tccagtgcct	caacgggggc cagcaacgac aaccactact tcggctacag caccctctgg 840
gggtattttg	atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900
atcaacaaca	attgggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960
gtcaaggagg	tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020
gttcaagtct	tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080
ggctgcctcc	ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140
ctcaacaatg	gcagccaagc cgtgggacgt tcattccttt actgcctgga atatttcct 1200
tctcagatgc	tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260
ttccacagca	gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320
caatacctgt	attaccgaa cagaactcaa aatcagtcgg gaagtgccta aaacaaggac 1380
ttgtgtttta	gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
ggaccctgtt	atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500
tttacctgga	ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta	tggcctcaca	caaagacgac	gaagacaagt	tctttcccat	gagcgggtgc	1620
atgatttttg	gaaaagagag	cgccggagct	tcaaacactg	cattggacaa	tgcatgatt	1680
acagacgaag	aggaaattaa	agccactaac	cctgtggcca	ccgaaagatt	tgggaccgtg	1740
gcagtcaatt	tccagagcag	cagcacagac	cctgcgaccg	gagatgtgca	tgctatggga	1800
gcattacctg	gcatggtgtg	gcaaggtaga	gacgtgtacc	tgcaagggtcc	catttgggcc	1860
aaaattcctc	acacagatgg	acactttcac	ccgtctcctc	ttatgggcgg	ctttggactc	1920
aagaaccgcg	ctcctcagat	cctcatcaaa	aacacgcctg	ttcctgcgaa	tcctccggcg	1980
gagttttcag	ctacaaagtt	tgcttcattc	atcacccaat	actccacagg	acaagtgagt	2040
gtggaaattg	aatgggagct	gcagaaagaa	aacagcaagc	gctggaatcc	cgaagtgcag	2100
tacacatcca	attatgcaaa	atctgccaac	gttgatttta	ctgtggacaa	caatggactt	2160
tatactgagc	ctcgcccat	tggcacccgt	taccttacct	gtcccctgta	a	2211

<210> 82  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.46

<400>	82					
atggctgccc	acggttatct	tccagattgg	ctcgaggaca	ctctctctga	aggaataaga	60
cagtgggtga	agctcaaacc	tggcccacca	ccaccaagc	ccgcagagcg	gcataaggac	120
gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gacccttcaa	cggactcgac	180
aaggagagc	cggatcaacg	ggcagacgcc	gcggccctcg	agcacgacaa	agcctacgac	240
cggcagctcg	acagcggaga	caaccgtac	ctcaagtaca	accacgccga	cgcggagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcgggcgggc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggt	ctgggtgagg	aaggcgctaa	gacggctcct	420
ggaaagaaac	gtccggtaga	gcagtcgcca	caagagccag	actccccctc	gggcatcggc	480
aagacaggcc	agcagccgcg	taaaaagaga	ctcaattttg	gtcagactgg	cgactcagag	540
tcagtccccg	atccacaacc	tctcggagaa	cctccagcaa	cccccgctgc	tgtgggacct	600
actacaatgg	cttcaggcgg	tggcgacca	atggcagaca	ataacgaagg	cgccgacgga	660
gtgggtaatg	cctcaggaaa	ttggcactgc	gattccacat	ggctgggcga	cagagtcac	720
accaccagca	ccgcacctg	ggccttgccc	acctacaata	accacctcta	caagcaaata	780
tccagtgttt	caacgggggc	cagcaacgac	aaccactact	tcggctacag	caccccttgg	840
gggtattttg	atttcaacag	attccactgc	cactttttcac	cacgtgactg	gcagcgactc	900
atcaacaaca	attgggggatt	ccggcccaag	agactcaact	tcaaactctt	caacatccaa	960
gtcaaggagg	tcacgacgaa	tgatggcgtc	acaaccatcg	ctaataacct	taccagcacg	1020
gttcaagtct	tctcggactc	ggagtaccag	cttccgtacg	tcctcggctc	tgcgaccacg	1080
ggccgcctcc	ctccgttccc	ggcggacgtg	ttcatgattc	cgcaatacgg	ctacctgacg	1140
ctcaacaatg	gcagccaagc	cgtgggacgt	tcattctctt	actgcctgga	atatttccct	1200
tctcagatgc	tgagaacggg	caacaacttt	accttcagct	acacctttga	ggaagtgcct	1260
ctccacagca	gctgcgcgca	cagccagagc	ctggaccggc	tgatgaatcc	tctcatcgac	1320
caatacctgt	attacctgaa	cagaactcaa	aatcagtcgg	gaagtgccca	aaacagggac	1380
ttgtctgtta	gccgtgggtc	tccagctggc	atgtctgttc	agcccaaaaa	ctggctacct	1440
ggaccctgtt	atcggcagca	gcgcgtttct	aaaacaaaaa	cagacaacaa	caacagcaat	1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560  
 ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgtc 1620  
 atgatttttg gaaaagagag cgccggagct tcaaactctg cattggacaa tgtcatgatt 1680  
 acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740  
 gcagtcgaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800  
 gcattaccctg gcatgggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860  
 aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920  
 aagaacccgc ctctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980  
 gagttttcag ctacaaagtt tgcttcattc atcacccaat actccgcagg acaagtgagt 2040  
 gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100  
 tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160  
 tatactgagc ctgcgcccat tggcaccctg taccttacct gtcccctgta a 2211

<210> 83  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.17

<400> 83

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 84  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.6

<400> 84

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Ala Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Pro Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 85  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.42

<400> 85

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220  
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Ser Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Leu  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 86  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.38

<400> 86

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Arg Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Pro Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 87  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.40  
 <400> 87

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Ser Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu

675

680

685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 88  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.37

<400> 88

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 Page 97

545                      550                      555                      560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
                                  565                                   570                                   575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
                                  580                                   585                                   590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
                                  595                                   600                                   605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
                                  610                                   615                                   620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
                                  625                                   630                                   635                                   640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
                                  645                                   650                                   655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
                                  660                                   665                                   670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
                                  675                                   680                                   685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
                                  690                                   695                                   700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
                                  705                                   710                                   715                                   720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
                                  725                                   730                                   735

Asn Leu

<210> 89  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.39

<400> 89

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
   1                                 5                                 10                                 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
                                  20                                 25                                 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
                                  35                                 40                                 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                                  50                                 55                                 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
   65                                 70                                 75                                 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
                                  85                                 90                                 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser

420                      425                      430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
                     435                      440                      445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
                     450                      455                      460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
                     465                      470                      475                      480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
                     485                      490                      495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
                     500                      505                      510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
                     515                      520                      525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
                     530                      535                      540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
                     545                      550                      555                      560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
                     565                      570                      575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
                     580                      585                      590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
                     595                      600                      605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
                     610                      615                      620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
                     625                      630                      635                      640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
                     645                      650                      655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
                     660                      665                      670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
                     675                      680                      685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
                     690                      695                      700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
                     705                      710                      715                      720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
                     725                      730                      735  
 Asn Leu

<210> 90  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone AAV4407

<400> 90

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn

290	295	300
Asn 305	Asn 310	Trp 315
Gly 320	Phe 325	Arg 330
Ile 335	Gln 340	Val 345
Asn 350	Asn 355	Leu 360
Leu 365	Pro 370	Tyr 375
Pro 385	Ala 390	Asp 395
Asn 400	Gly 405	Ser 410
Phe 415	Pro 420	Ser 425
Thr 430	Phe 435	Glu 440
Leu 445	Asp 450	Arg 455
Ser 460	Thr 465	Gln 470
Phe 475	Ser 480	Gln 485
Leu 490	Pro 495	Val 500
Gln 505	Asn 510	Thr 515
Leu 520	Asn 525	Val 530
His 535	Lys 540	Asp 545
Phe 550	Gly 555	Val 560
Met 565	Leu 570	Thr 575
Glu 580	Gln 585	Tyr 590
Pro 595	Ile 600	Val 605
Trp 610	Gln 615	Arg 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 91  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.41

<400> 91

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Pro Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln



Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 92  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.40

<400> 92

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 Page 105

35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
   50                      55                      60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
   65                      70                      75                      80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
                     85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
                     100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                     115                      120                      125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
   130                      135                      140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
   145                      150                      155                      160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
                     165                      170                      175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
                     180                      185                      190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
                     195                      200                      205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
   210                      215                      220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
   225                      230                      235                      240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
                     245                      250                      255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
                     260                      265                      270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
                     275                      280                      285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
   290                      295                      300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
   305                      310                      315  
 Ile Gln Val Lys Glu Val Thr Gln Asp Glu Gly Thr Lys Thr Ile Ala  
                     325                      330                      335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
                     340                      345                      350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
                     355                      360                      365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Arg Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu  
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 93  
<211> 731  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone pi.1

<400> 93

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln  
145 150 155 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser  
165 170 175

Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly  
180 185 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp  
195 200 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His  
210 215 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg  
225 230 235 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser  
 245 250 255  
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350  
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val  
 370 375 380  
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn  
 420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn  
 435 440 445  
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln  
 450 455 460  
 Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg  
 465 470 475 480  
 Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe  
 485 490 495  
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu  
 500 505 510  
 Val Ser Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg  
 515 520 525  
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly  
 530 535 540  
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu  
 545 550 555 560  
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala  
 565 570 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn  
580 585 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr  
595 600 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe  
610 615 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro  
625 630 635 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn  
645 650 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly  
660 665 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys  
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala  
690 695 700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg  
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730

<210> 94  
<211> 731  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone pi.3

<400> 94

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln  
 145 150 155 160  
 Pro Ala Lys Lys Arg Leu Asn Phe Gly Pro Thr Gly Asp Ser Glu Ser  
 165 170 175  
 Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly  
 180 185 190  
 Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp  
 195 200 205  
 Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His  
 210 215 220  
 Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg  
 225 230 235 240  
 Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser  
 245 250 255  
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Gln Asn Glu Gly Thr Lys Thr Thr Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350  
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val  
 370 375 380  
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn  
 420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn  
 435 440 445  
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln  
 450 455 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg  
465 470 475 480

Gln Gln Arg Val Ser Thr Ala Val Ser Gln Asn Asn Asn Ser Asn Phe  
485 490 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu  
500 505 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg  
515 520 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly  
530 535 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu  
545 550 555 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala  
565 570 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn  
580 585 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr  
595 600 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe  
610 615 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro  
625 630 635 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn  
645 650 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly  
660 665 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys  
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala  
690 695 700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg  
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730

<210> 95  
<211> 731  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone pi.2

<400> 95

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Arg Gln  
 145 150 155 160  
 Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser  
 165 170 175  
 Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly  
 180 185 190  
 Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp  
 195 200 205  
 Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His  
 210 215 220  
 Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg  
 225 230 235 240  
 Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser  
 245 250 255  
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Thr Asp Ser Lys Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val  
 370 375 380  
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn  
 420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn  
 435 440 445  
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln  
 450 455 460  
 Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg  
 465 470 475 480  
 Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe  
 485 490 495  
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu  
 500 505 510  
 Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg  
 515 520 525  
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly  
 530 535 540  
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu  
 545 550 555 560  
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala  
 565 570 575  
 Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn  
 580 585 590  
 Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr  
 595 600 605  
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe  
 610 615 620  
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro  
 625 630 635 640  
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn  
 645 650 655  
 Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly  
 660 665 670  
 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys  
 675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala  
690 695 700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg  
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730

<210> 96  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.52

<400> 96

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Ser Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Ser Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 97  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.53

<400> 97

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Val His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Ser Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg  
 725 730 735  
 Asn Leu

<210> 98  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>

<223> vp1, clone rh.70

<400> 98

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220  
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Ala Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270  
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285  
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300  
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Ser Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val

645                      650                      655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Ser  
                     660                      665                      670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
                     675                      680                      685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
                     690                      695                      700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
                     705                      710                      715                      720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
                     725                      730                      735

Asn Leu

<210> 99  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.64

<400> 99

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1                      5                      10                      15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
                     20                      25                      30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
                     35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                     50                      55                      60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
                     85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
                     100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                     115                      120                      125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
                     130                      135                      140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145                      150                      155                      160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
                     165                      170                      175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
                     180                      185                      190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 Page 123

515                      520                      525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
     530                      535                      540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
     545                      550                      555                      560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
                     565                      570                      575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
                     580                      585                      590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
                     595                      600                      605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
     610                      615                      620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
     625                      630                      635                      640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
                     645                      650                      655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
                     660                      665                      670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu  
                     675                      680                      685  
 Leu Gln Lys Glu Asn Ser Lys Arg Arg Asn Pro Glu Ile Gln Tyr Thr  
     690                      695                      700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
     705                      710                      715                      720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
                     725                      730                      735

Asn Leu

<210> 100  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.68

<400> 100

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
     1                      5                      10                      15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
                     20                      25                      30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
                     35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
     50                      55                      60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 Page 125

385                      390                      395                      400  
 Phe Pro Ser Gln Met<sub>405</sub> Leu Arg Thr Gly<sub>410</sub> Asn<sub>410</sub> Phe Ser Phe<sub>415</sub> Ser Tyr  
 Thr Phe Glu Asp<sub>420</sub> Val Pro Phe His Ser<sub>425</sub> Ser Tyr Ala His Ser<sub>430</sub> Gln Ser  
 Leu Asp Arg<sub>435</sub> Leu Met Asn Pro<sub>440</sub> Leu Ile Asp Gln Tyr<sub>445</sub> Leu Tyr Tyr Leu  
 Ser Arg Thr Gln Ser Thr Gly<sub>455</sub> Gly Thr Ala Gly Thr<sub>460</sub> Gln Gln Leu Leu  
 Phe Ser Gln Ala Gly<sub>470</sub> Pro Ser Asn Met Ser<sub>475</sub> Ala Gln Ala Arg Asn Trp<sub>480</sub>  
 Leu Pro Gly Pro Cys<sub>485</sub> Tyr Arg Gln Gln Arg<sub>490</sub> Val Ser Thr Thr<sub>495</sub> Leu Ser  
 Gln Asn Asn<sub>500</sub> Ser Asn Phe Ala Trp<sub>505</sub> Thr Gly Ala Thr Lys<sub>510</sub> Tyr His  
 Leu Asn Gly<sub>515</sub> Arg Asp Ser Leu Val<sub>520</sub> Asn Pro Gly Val<sub>525</sub> Ala Met Ala Thr  
 Asn Lys<sub>530</sub> Asp Asp Glu Asp Arg<sub>535</sub> Phe Phe Pro Pro<sub>540</sub> Ser Gly Ile Leu Met  
 Phe Gly Lys Gln Gly<sub>550</sub> Ala Gly Lys Asp Asn Val<sub>555</sub> Asp Tyr Ser Asn Val<sub>560</sub>  
 Met Leu Thr Ser<sub>565</sub> Glu Glu Glu Ile Lys Thr<sub>570</sub> Thr Asn Pro Val<sub>575</sub> Ala Thr  
 Glu Gln Tyr Gly<sub>580</sub> Val Val Ala Asp Asn<sub>585</sub> Leu Gln Gln Gln Asn<sub>590</sub> Thr Ala  
 Pro Ile Val<sub>595</sub> Gly Ala Val Asn Ser<sub>600</sub> Gln Gly Ala Leu Pro<sub>605</sub> Gly Met Val  
 Trp Gln Asn Arg Asp Val Tyr<sub>615</sub> Leu Gln Gly Pro<sub>620</sub> Ile Trp Ala Lys Ile  
 Pro His Thr Asp Gly<sub>630</sub> Asn Phe His Pro Ser<sub>635</sub> Leu Met Gly Gly Phe<sub>640</sub>  
 Gly Leu Lys His Pro<sub>645</sub> Pro Pro Gln Ile Leu<sub>650</sub> Ile Lys Asn Thr Pro<sub>655</sub> Val  
 Pro Ala Asp Pro<sub>660</sub> Pro Thr Ala Phe Asn<sub>665</sub> Gln Ala Lys Leu Asn<sub>670</sub> Ser Phe  
 Ile Thr Gln Tyr Ser Thr Gly<sub>680</sub> Gln Val Ser Val Val<sub>685</sub> Ile Glu Trp Glu  
 Leu Gln Lys Glu Asn Ser Lys<sub>695</sub> Arg Trp Asn Pro Glu<sub>700</sub> Ile Gln Tyr Thr  
 Ser Asn Tyr Tyr Lys Ser<sub>710</sub> Thr Asn Val Asp Phe<sub>715</sub> Ala Val Asn Thr Glu<sub>720</sub>

Gly Val Tyr Ser Glu Leu Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 101  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.46

<400> 101

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp

260							265							270						
Asn	Thr	Tyr <sub>275</sub>	Phe	Gly	Tyr	Ser	Thr <sub>280</sub>	Pro	Trp	Gly	Tyr	Phe <sub>285</sub>	Asp	Phe	Asn					
Arg	Phe <sub>290</sub>	His	Cys	His	Phe	Ser <sub>295</sub>	Pro	Arg	Asp	Trp	Gln <sub>300</sub>	Arg	Leu	Ile	Asn					
Asn <sub>305</sub>	Asn	Trp	Gly	Phe	Arg <sub>310</sub>	Pro	Lys	Arg	Leu	Ser <sub>315</sub>	Phe	Lys	Leu	Phe	Asn <sub>320</sub>					
Ile	Gln	Val	Lys	Glu <sub>325</sub>	Val	Thr	Gln	Asn	Glu <sub>330</sub>	Gly	Thr	Lys	Thr	Ile <sub>335</sub>	Ala					
Asn	Asn	Leu	Thr <sub>340</sub>	Ser	Thr	Ile	Gln	Val <sub>345</sub>	Phe	Thr	Asp	Ser	Glu <sub>350</sub>	Tyr	Gln					
Leu	Pro	Tyr <sub>355</sub>	Val	Leu	Gly	Ser	Ala <sub>360</sub>	His	Gln	Gly	Cys	Leu <sub>365</sub>	Pro	Pro	Phe					
Pro	Ala <sub>370</sub>	Asp	Val	Phe	Met	Ile <sub>375</sub>	Pro	Gln	Tyr	Gly	Tyr <sub>380</sub>	Leu	Thr	Leu	Asn					
Asn <sub>385</sub>	Gly	Ser	Gln	Ala	Val <sub>390</sub>	Gly	Arg	Ser	Ser	Phe <sub>395</sub>	Tyr	Cys	Leu	Glu	Tyr <sub>400</sub>					
Phe	Pro	Ser	Gln	Met <sub>405</sub>	Leu	Arg	Thr	Gly	Asn <sub>410</sub>	Asn	Phe	Ser	Phe	Ser <sub>415</sub>	Tyr					
Thr	Phe	Glu	Asp <sub>420</sub>	Val	Pro	Phe	His	Ser <sub>425</sub>	Ser	Tyr	Ala	His	Ser <sub>430</sub>	Gln	Ser					
Leu	Asp	Arg <sub>435</sub>	Leu	Met	Asn	Pro	Leu <sub>440</sub>	Ile	Asp	Gln	Tyr	Leu <sub>445</sub>	Tyr	Tyr	Leu					
Ser	Arg <sub>450</sub>	Thr	Gln	Ser	Thr	Gly <sub>455</sub>	Gly	Thr	Ala	Gly	Thr <sub>460</sub>	Gln	Gln	Leu	Leu					
Phe <sub>465</sub>	Ser	Gln	Ala	Gly	Pro <sub>470</sub>	Ser	Asn	Met	Ser	Ala <sub>475</sub>	Gln	Ala	Arg	Asn	Trp <sub>480</sub>					
Leu	Pro	Gly	Pro	Cys <sub>485</sub>	Tyr	Arg	Gln	Gln	Arg <sub>490</sub>	Val	Ser	Thr	Thr	Leu <sub>495</sub>	Ser					
Gln	Asn	Asn	Asn <sub>500</sub>	Ser	Asn	Phe	Ala	Trp <sub>505</sub>	Thr	Gly	Ala	Thr	Lys <sub>510</sub>	Tyr	His					
Leu	Asn	Gly <sub>515</sub>	Arg	Asp	Ser	Leu	Val <sub>520</sub>	Asn	Pro	Gly	Val	Ala <sub>525</sub>	Met	Ala	Thr					
Asn	Lys <sub>530</sub>	Asp	Asp	Glu	Asp	Arg <sub>535</sub>	Phe	Phe	Pro	Ser	Ser <sub>540</sub>	Gly	Ile	Leu	Met					
Phe <sub>545</sub>	Gly	Lys	Gln	Gly	Ala <sub>550</sub>	Gly	Lys	Asp	Asn	Val <sub>555</sub>	Asp	Tyr	Ser	Asn	Val <sub>560</sub>					
Met	Leu	Thr	Ser	Glu <sub>565</sub>	Glu	Glu	Ile	Lys	Ala <sub>570</sub>	Thr	Asn	Pro	Val	Ala <sub>575</sub>	Thr					
Glu	Gln	Tyr	Gly <sub>580</sub>	Val	Val	Ala	Asp	Asn <sub>585</sub>	Leu	Gln	Gln	Gln	Asn <sub>590</sub>	Thr	Ala					

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 102  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.39

<400> 102

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
Page 129

130	135	140
Pro Val Glu Pro Ser	Pro Gln Arg Ser	Pro Asp Ser Ser Thr Gly Ile
145	150	155 160
Gly Lys Lys Gly	Gln Gln Pro Ala Arg	Lys Arg Leu Asn Phe Gly Arg
	165	170 175
Thr Gly Asp Ser	Glu Ser Val Pro	Asp Pro Gln Pro Ile Gly Glu Pro
	180	185 190
Pro Ala Ala Pro Ser Ser Val	Gly Ser Gly Thr Met	Ala Ala Gly Gly
	195 200	205
Gly Ala Pro Met Ala Asp	Asn Asn Glu Gly Ala	Asp Gly Val Gly Ser
	210 215	220
Ser Ser Gly Asn Trp	His Cys Asp Ser Thr	Trp Leu Gly Asp Arg Val
	225 230	235 240
Ile Thr Thr Ser	Thr Arg Thr Trp Ala	Leu Pro Thr Tyr Asn Asn His
	245	250 255
Leu Tyr Lys Gln Ile Ser Asn Gly	Thr Ser Gly Gly Ser	Thr Asn Asp
	260 265	270
Asn Thr Tyr Phe Gly Tyr Ser	Thr Pro Trp Gly Tyr	Leu Asp Phe Asn
	275 280	285
Arg Phe His Cys His Phe	Ser Pro Arg Asp Trp	Gln Arg Leu Ile Asn
	290 295	300
Asn Asn Trp Gly Phe Arg	Pro Lys Arg Leu Ser	Phe Lys Leu Phe Asn
	305 310	315 320
Ile Gln Val Lys Glu Val Thr Gln	Asn Glu Gly Thr Lys Thr	Ile Ala
	325 330	335
Asn Asn Leu Ala Ser Thr Ile Gln	Val Phe Thr Asp Ser	Glu Tyr Gln
	340 345	350
Pro Pro Tyr Val Leu Gly Ser	Ala His Gln Gly Cys	Leu Pro Pro Phe
	355 360	365
Pro Ala Asp Val Phe Met	Ile Pro Gln Tyr Gly	Tyr Leu Thr Leu Asn
	370 375	380
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser	Phe Tyr Cys Leu Glu Tyr	
	385 390	395 400
Phe Pro Ser Gln Met	Leu Arg Thr Gly	Asn Asn Phe Ser Phe Ser Tyr
	405	410 415
Thr Phe Glu Asp Val Pro Phe His	Ser Ser Tyr Ala His	Ser Gln Ser
	420 425	430
Leu Asp Arg Leu Met Asn Pro	Leu Ile Asp Gln Tyr	Leu Tyr Tyr Leu
	435 440	445
Ser Arg Thr Gln Ser Thr	Gly Gly Thr Ala Gly	Thr Gln Gln Leu Leu
	450 455	460

Phe Ser Arg Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Thr Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Ala Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Ala Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 103  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.49

<400> 103

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

1	5	10	15
Glu Gly Ile Arg	Glu Trp Trp Asp	Leu Lys Pro Gly	Ala Pro Lys Pro
20	25	30	
Lys Ala Asn Gln Gln Lys Gln	Asp Asp Gly Arg Gly	Leu Val Leu Pro	
35	40	45	
Gly Tyr Lys Tyr Leu Gly	Pro Phe Asn Gly	Leu Asp Lys Gly	Glu Pro
50	55	60	
Val Asn Ala Ala Asp	Ala Ala Ala Leu Glu	His Asp Lys Ala Tyr	Asp
65	70	75	80
Gln Gln Leu Lys	Ala Gly Asp Asn Pro	His Leu Arg Tyr Asn	His Ala
85	90	95	
Asp Ala Glu Phe Gln Glu Arg	Leu Gln Glu Asp Thr Ser	Phe Gly Gly	
100	105	110	
Asn Leu Gly Arg Ala Val Phe	Gln Ala Lys Lys Arg	Val Leu Glu Pro	
115	120	125	
Leu Gly Leu Val Glu Glu Gly	Ala Lys Thr Ala Pro	Gly Lys Lys Arg	
130	135	140	
Pro Val Glu Pro Ser	Pro Gln Arg Ser Pro	Asp Ser Ser Thr Gly	Ile
145	150	155	160
Gly Lys Lys Gly Gln Gln Pro	Ala Arg Lys Arg Leu Asn Phe	Gly Gln	
165	170	175	
Thr Gly Asp Ser	Glu Ser Val Pro Asp	Pro Gln Leu Ile Gly	Glu Pro
180	185	190	
Pro Ala Ala Pro Ser Ser Val	Gly Ser Gly Thr Met	Ala Ala Gly Gly	
195	200	205	
Gly Ala Pro Met Ala Asp	Asn Asn Glu Gly Ala	Asp Gly Val Gly Ser	
210	215	220	
Ser Ser Gly Asn Trp His	Cys Asp Ser Thr Trp	Leu Gly Asp Arg Val	
225	230	235	240
Ile Thr Thr Ser Thr Arg Thr Trp	Ala Leu Pro Thr Tyr Asn	Asn His	
245	250	255	
Leu Tyr Lys Gln Ile Ser Asn Gly	Thr Ser Gly Gly Ser Thr	Asn Asp	
260	265	270	
Asn Thr Tyr Phe Gly Tyr Ser	Thr Pro Trp Gly Tyr Phe	Asp Phe Asn	
275	280	285	
Arg Phe His Cys His Phe	Ser Pro Arg Asp Trp Gln	Arg Leu Ile Asn	
290	295	300	
Asn Asn Trp Gly Phe Arg	Pro Lys Arg Leu Ser	Phe Lys Leu Phe Asn	
305	310	315	320
Ile Gln Val Lys Glu Val Thr Gln	Asn Glu Gly Thr Lys Thr	Ile Ala	
325	330	335	

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Asn Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Met Gly Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670

Ile Thr Gln Tyr Gly Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 104  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.51

<400> 104

Met Val Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Leu Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Gln Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Pro Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 105  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.57

<400> 105

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Thr Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Ala Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735  
 Asn Leu

<210> 106  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.58

<400> 106

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val  
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
675 680 685

Leu Gln Lys Glu Asn Ser Lys Cys Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 107  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.61

<400> 107

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Pro Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Pro Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asp Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Val Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 108  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.50

<400> 108

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Gly Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Ser Pro Glu Ile Gln Tyr Thr  
 Page 145

690

695

700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 109  
<211> 737  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.45

<400> 109

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser  
 435 440 445  
 Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe  
 450 455 460  
 Ser Gln Ala Gly Pro Ser Asn Met Ser Thr Gln Ala Arg Asn Trp Leu  
 465 470 475 480  
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln  
 485 490 495  
 Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu  
 500 505 510  
 Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr Asn  
 515 520 525  
 Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met Phe  
 530 535 540  
 Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val Met  
 545 550 555 560  
 Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu

565                      570                      575  
 Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro  
                                  580                      585                      590  
 Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp  
                                  595                      600                      605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
                                  610                      615                      620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
                                  625                      630                      635                      640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
                                  645                      650                      655  
 Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile  
                                  660                      665                      670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
                                  675                      680                      685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
                                  690                      695                      700  
 Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly  
                                  705                      710                      715                      720  
 Ala Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
                                  725                      730                      735

Leu

<210> 110  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.59

<400> 110

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1                      5                      10                      15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
                                  20                      25                      30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
                                  35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                                  50                      55                      60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
                                  85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
                                  100                      105                      110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Pro Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 Page 149

435	440	445
Arg Thr Gln Ser Asn Ala Gly 450	Gly Thr Ala Gly 455	Asn Arg Glu Leu Gln 460
Phe Tyr Gln Gly Gly 465	Pro Thr Thr Met Ala 470	Glu Gln Ala Lys Asn Trp 475 480
Leu Pro Gly Pro 485	Cys Tyr Arg Gln Gln 490	Val Ser Thr Thr Leu Ser 495
Gln Asn Asn Asn 500	Ser Asn Phe Ala Trp 505	Thr Gly Ala Thr Lys Tyr His 510
Leu Asn Gly 515	Arg Asp Ser Leu Val 520	Asn Pro Gly Val Ala Met Ala Thr 525
Asn Lys Asp Asp Glu Asp 530	Arg Phe Phe Pro Ser 535	Ser Gly Ile Leu Met 540
Phe Gly Lys Gln Gly 545	Ala Gly Lys Asp Asn Val 550	Asp Tyr Ser Asn Val 555 560
Met Leu Thr Ser 565	Glu Glu Glu Ile Lys Thr 570	Thr Asn Pro Val Ala Thr 575
Glu Gln Tyr 580	Gly Val Val Ala Asp Asn 585	Leu Gln Gln Gln Asn Thr Ala 590
Pro Ile Val 595	Gly Ala Val Asn Ser 600	Gln Gly Ala Leu Pro Gly Met Val 605
Trp Gln Asn Arg Asp Val 610	Tyr Leu Gln Gly Pro 615	Ile Trp Ala Lys Ile 620
Pro His Thr Asp Gly 625	Asn Phe His Pro Ser 630	Pro Leu Met Gly Gly Phe 635 640
Gly Leu Lys His 645	Pro Pro Gln Ile Leu 650	Ile Lys Asn Thr Pro Val 655
Pro Ala Asp Pro 660	Pro Thr Ala Phe Asn 665	Gln Ala Lys Leu Asn Ser Phe 670
Ile Thr Gln Tyr Ser Thr Gly 675	Gln Val Ser Val Glu 680	Ile Glu Trp Glu 685
Leu Gln Lys Glu Asn Ser 690	Lys Arg Trp Asn Pro 695	Glu Ile Gln Tyr Thr 700
Ser Asn Tyr Tyr Lys 705	Ser Thr Asn Val Asp 710	Phe Ala Val Asn Thr Glu 715 720
Gly Val Tyr Ser 725	Glu Pro Arg Pro Ile Gly 730	Thr Arg Tyr Leu Thr Arg 735

Asn Leu

<210> 111  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>

<223> vp1, clone rh.44

<400> 111

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Cys Asp  
65 70 75 80  
Gln Arg Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
210 215 220  
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
260 265 270  
Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
275 280 285  
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
290 295 300  
Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile

305		310		315		320
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn						
		325		330		335
Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu						
		340		345		350
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro						
		355		360		365
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn						
		370		375		380
Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe						
		385		390		395
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr						
		405		410		415
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu						
		420		425		430
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala						
		435		440		445
Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln						
		450		455		460
Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp						
		465		470		475
Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp						
		485		490		495
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His						
		500		505		510
Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr						
		515		520		525
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile						
		530		535		540
Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu						
		545		550		555
Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu						
		565		570		575
Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala						
		580		585		590
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp						
		595		600		605
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro						
		610		615		620
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly						
		625		630		635
				640		

Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Glu Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 112  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.65

<400> 112

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro

180	185	190
Pro Ala Gly 195	Pro Ser Gly Leu Gly 200	Ser Gly Thr Met Ala Ala Gly Gly 205
Gly Ala Pro Met Ala Asp 210	Asn Asn Glu Gly Ala Asp 215 220	Gly Val Gly Asn
Ala Ser Gly Asn Trp 225	His Cys Asp Ser Thr 230 235	Trp Leu Gly Asp Arg Val 240
Ile Thr Thr Ser Thr 245	Arg Thr Trp Ala Leu 250	Pro Thr Tyr Asn Asn His 255
Leu Tyr Lys Gln 260	Ile Ser Ser Gln Ser 265	Ala Gly Ser Thr Asn Asp Asn 270
Val Tyr Phe Gly Tyr Ser Thr 275	Pro Trp Gly Tyr Phe Asp 280 285	Phe Asn Arg
Phe His Cys His Phe Ser 290	Pro Arg Asp Trp Gln Arg 295 300	Leu Ile Asn Asn
Asn Trp Gly Phe Arg Pro 305	Lys Lys Leu Asn Phe Lys 310 315	Leu Phe Asn Ile 320
Gln Val Lys Glu Val Thr Thr 325	Asn Asp Gly Val Thr Thr 330	Ile Ala Asn 335
Asn Leu Thr Ser Thr Val Gln Val 340	Phe Ser Asp Ser Glu Tyr Gln Leu 345 350	
Pro Tyr Val Leu Gly Ser Ala 355	His Gln Gly Cys Leu Pro 360 365	Pro Phe Pro
Ala Asp Val Phe Met Ile Pro 370	Gln Tyr Gly Tyr Leu Thr Leu Asn Asn 375 380	
Gly Ser Gln Ser Val Gly 385	Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe 390 395	400
Pro Ser Gln Met Leu Arg Thr Gly 405	Asn Asn Phe Thr Phe Ser Tyr Thr 410 415	
Phe Glu Asp Val Pro Phe His Ser 420	Ser Tyr Ala His Ser Gln Ser Leu 425 430	
Asp Arg Leu Met Asn Pro Leu Ile 435	Asp Gln Tyr Leu Tyr Tyr Leu Ala 440 445	
Arg Thr Gln Ser Asn Ala Gly 450	Gly Thr Ala Gly Asn Arg Glu Leu Gln 455 460	
Phe Tyr Gln Gly Gly Pro Thr Thr 465	Met Ala Glu Gln Ala Lys Asn Trp 470 475	480
Leu Pro Arg Pro Cys Phe Arg Gln Gln 485	Arg Val Ser Lys Thr Leu Asp 490 495	
Gln Asn Asn Asn Ser Asn Phe Ala Trp 500	Thr Gly Ala Thr Lys Tyr His 505 510	

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 113  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.67

<400> 113

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 Page 155

50	55	60
Val <sub>65</sub> Asn Ala Ala Asp <sub>70</sub> Ala Ala Leu Glu <sub>75</sub> His <sub>75</sub> Asp Lys Ala Tyr Asp <sub>80</sub>		
Gln Gln Leu Lys <sub>85</sub> Ala Gly Asp Asn Pro Tyr <sub>90</sub> Leu Arg Tyr Asn His <sub>95</sub> Ala		
Asp Ala Glu Phe <sub>100</sub> Gln Glu Arg Leu <sub>105</sub> Gln Glu Asp Thr Ser Phe <sub>110</sub> Gly Gly		
Asn Leu Gly <sub>115</sub> Arg Ala Val Leu <sub>120</sub> Gln Ala Lys Lys Arg Val <sub>125</sub> Leu Glu Pro		
Leu Gly <sub>130</sub> Leu Val Glu Glu <sub>135</sub> Ala Ala Lys Thr Ala <sub>140</sub> Pro Gly Lys Lys Arg		
Pro Val <sub>145</sub> Glu Pro Ser <sub>150</sub> Pro Gln Arg Ser Pro <sub>155</sub> Asp Ser Ser Thr Gly <sub>160</sub> Ile		
Gly Lys Lys Gly <sub>165</sub> Gln Gln Pro Ala Arg Lys <sub>170</sub> Arg Leu Asn Phe Gly <sub>175</sub> Gln		
Thr Gly Asp <sub>180</sub> Ser Glu Ser Val Pro <sub>185</sub> Asp Pro Gln Pro Ile Gly <sub>190</sub> Glu Pro		
Pro Ala Gly <sub>195</sub> Pro Ser Gly Leu <sub>200</sub> Gly Ser Gly Thr Met <sub>205</sub> Ala Ala Gly Gly		
Gly Ala <sub>210</sub> Pro Met Ala Asp <sub>215</sub> Asn Asn Glu Gly Ala <sub>220</sub> Asp Gly Val Gly Asn		
Ala Ser Gly Asn Trp <sub>230</sub> His Cys Asp Ser Thr <sub>235</sub> Trp Leu Gly Asp Arg Val <sub>240</sub>		
Ile Thr Thr Ser <sub>245</sub> Thr Arg Thr Trp Ala <sub>250</sub> Leu Pro Thr Tyr Asn <sub>255</sub> Asn His		
Leu Tyr Lys <sub>260</sub> Gln Ile Ser Ser Gln <sub>265</sub> Ser Ala Gly Ser Thr Asn <sub>270</sub> Asp Asn		
Val Tyr Phe <sub>275</sub> Gly Tyr Ser Thr <sub>280</sub> Pro Trp Gly Tyr Phe <sub>285</sub> Asp Phe Asn Arg		
Phe His <sub>290</sub> Cys His Phe Ser <sub>295</sub> Pro Arg Asp Trp Gln <sub>300</sub> Arg Leu Ile Asn Asn		
Asn Trp Gly Phe Arg <sub>310</sub> Pro Lys Lys Leu Asn <sub>315</sub> Phe Lys Leu Phe Asn <sub>320</sub> Ile		
Gln Val Lys Glu <sub>325</sub> Val Thr Thr Asn Asp <sub>330</sub> Gly Val Thr Thr Ile <sub>335</sub> Ala Asn		
Asn Leu Thr <sub>340</sub> Ser Thr Val Gln Val <sub>345</sub> Phe Ser Asp Ser Glu <sub>350</sub> Tyr Gln Leu		
Pro Tyr Val <sub>355</sub> Leu Gly Ser Ala <sub>360</sub> His Gln Gly Cys Leu <sub>365</sub> Pro Pro Phe Pro		
Ala Asp <sub>370</sub> Val Phe Met Ile <sub>375</sub> Pro Gln Tyr Gly Tyr <sub>380</sub> Leu Thr Leu Asn Asn		

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
725 730 735

Leu

<210> 114  
<211> 737  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.62

<400> 114

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Ala Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn  
210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Gly Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Asp Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 115  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.48

<400> 115

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 116  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.54  
 <400> 116

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
180 185 190  
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
210 215 220  
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
260 265 270  
Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
275 280 285  
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
290 295 300  
Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320  
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Val Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ser Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
675 680 685  
Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
690 695 700  
Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
705 710 715 720  
Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
725 730 735

Leu

<210> 117  
<211> 737  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.55

<400> 117

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Arg Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 118  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.47

<400> 118

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys His Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr  
 405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ala Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu  
 450 455 460  
 Gln Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn  
 465 470 475 480  
 Trp Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu  
 485 490 495  
 Asp Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr  
 500 505 510  
 His Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala  
 515 520 525  
 Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu  
 530 535 540  
 Ile Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val  
 545 550 555 560  
 Leu Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala  
 580 585 590  
 Ala Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 119  
<211> 737  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.69

<400> 119

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
210 215 220  
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
260 265 270  
Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
290 295 300  
Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320  
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
325 330 335  
Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
340 345 350  
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
355 360 365  
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
370 375 380  
Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
385 390 395 400  
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Ile Ser Tyr Thr  
405 410 415  
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430  
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
435 440 445  
Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Gln Glu Leu Gln  
450 455 460  
Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
465 470 475 480  
Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
485 490 495  
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
500 505 510  
Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
515 520 525  
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
530 535 540  
Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
545 550 555 560  
Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
565 570 575  
Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
580 585 590  
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
595 600 605  
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro

610                      615                      620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625                      630                      635                      640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
                     645                      650                      655  
 Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile  
                     660                      665                      670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
                     675                      680                      685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
                     690                      695                      700  
 Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly  
 705                      710                      715                      720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
                     725                      730                      735

Leu

<210> 120  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.60

<400> 120

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1                      5                      10                      15  
 Glu Gly Ile His Glu Trp Trp Asp Pro Lys Pro Gly Ala Pro Lys Pro  
                     20                      25                      30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
                     35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                     50                      55                      60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
                     85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
                     100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                     115                      120                      125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
                     130                      135                      140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145                      150                      155                      160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr His Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Glu Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser



Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
 145 150 155 160  
 Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
 260 265 270  
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp  
 Page 175

370	375	380
Gly 385	Gly 390	Tyr 395
Gly Gln Ala Val	Arg Ser Ser Phe	Cys Leu Glu Tyr Phe
Pro Ser Gln Met	Leu Arg Thr Gly Asn	Asn Phe Gln Phe Ser Tyr Glu
Phe Glu Asn Val	Pro Phe His Ser	Tyr Ala His Ser Gln Ser Leu
Asp Arg Leu Met	Asn Pro Leu Ile	Asp Gln Tyr Leu Tyr Tyr Leu Ser
Lys Thr Ile Asn Gly	Ser Gly Gln Asn Gln Gln Thr	Leu Lys Phe Ser
Val Ala Gly Pro Ser	Asn Met Ala Val	Gln Gly Arg Asn Tyr Ile Pro
Gly Pro Ser Tyr	Arg Gln Gln Arg Val	Ser Thr Thr Val Thr Gln Asn
Asn Asn Ser Glu	Phe Ala Trp Pro Gly	Ala Ser Ser Trp Ala Leu Asn
Gly Arg Asn Ser	Leu Met Asn Pro Gly	Pro Ala Met Ala Ser His Lys
Glu Gly Glu Asp	Arg Phe Phe Pro Leu Ser	Gly Ser Leu Ile Phe Gly
Lys Gln Gly Thr	Gly Arg Asp Asn Val	Asp Ala Asp Lys Val Met Ile
Thr Asn Glu Glu	Glu Ile Lys Thr Thr	Asn Pro Val Ala Thr Glu Ser
Tyr Gly Gln Val	Ala Thr Asn His	Gln Ser Ala Gln Ala Gln Ala Gln
Thr Gly Trp Val	Gln Asn Gln Gly	Ile Leu Pro Gly Met Val Trp Gln
Asp Arg Asp Val	Tyr Leu Gln Gly	Pro Ile Trp Ala Lys Ile Pro His
Thr Asp Gly Asn	Phe His Pro Ser Pro	Leu Met Gly Gly Phe Gly Met
Lys His Pro Pro	Pro Gln Ile Leu Ile	Lys Asn Thr Pro Val Pro Ala
Asp Pro Pro Thr	Ala Phe Asn Lys	Asp Lys Leu Asn Ser Phe Ile Thr
Gln Tyr Ser Thr	Gly Gln Val Ser	Val Glu Ile Glu Trp Glu Leu Gln
Lys Glu Asn Ser	Lys Arg Trp Asn	Pro Glu Ile Gln Tyr Thr Ser Asn

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val  
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 122  
<211> 736  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.32

<400> 122

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly  
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn

260	265	270
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg		
275	280	285
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn		
290	295	300
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile		
305	310	315
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn		
325	330	335
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu		
340	345	350
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro		
355	360	365
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp		
370	375	380
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe		
385	390	395
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu		
405	410	415
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu		
420	425	430
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser		
435	440	445
Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser		
450	455	460
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro		
465	470	475
Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn		
485	490	495
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn		
500	505	510
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys		
515	520	525
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly		
530	535	540
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile		
545	550	555
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser		
565	570	575
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln		
580	585	590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln  
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr  
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val  
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 123  
<211> 736  
<212> PRT  
<213> Unknown

<220>  
<223> capsid of hu.14/AAV9

<400> 123

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro  
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly

145	150	155	160
Lys Ser Gly Ala Gln 165	Pro Ala Lys Lys	Arg Leu Asn Phe Gly Gln 170 175	Thr
Gly Asp Thr Glu Ser Val 180	Pro Asp Pro Gln Pro Ile Gly Glu 185 190	Pro Pro	
Ala Ala Pro Ser Gly Val Gly 195 200	Leu Thr Met Ala Ser Gly Gly Gly	205	
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser 210 215 220			
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile 225 230 235 240			
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 245 250 255			
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn 260 265 270			
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg 275 280 285			
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn 290 295 300			
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile 305 310 315 320			
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn 325 330 335			
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu 340 345 350			
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro 355 360 365			
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp 370 375 380			
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe 385 390 395 400			
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu 405 410 415			
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu 420 425 430			
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser 435 440 445			
Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser 450 455 460			
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro 465 470 475 480			

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys  
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln  
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr  
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val  
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 124  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.33

<400> 124

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
Page 181

35	40	45
Gly Tyr Lys Tyr Leu Gly	Pro Phe Asn Gly Leu	Asp Lys Gly Glu Pro
50	55	60
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp		
65	70	75
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala		
	85	90
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly		
	100	105
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro		
	115	120
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg		
	130	135
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly		
	145	150
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr		
	165	170
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro		
	180	185
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly		
	195	200
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser		
	210	215
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile		
	225	230
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu		
	245	250
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr		
	260	265
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His		
	275	280
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp		
	290	295
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val		
	305	310
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu		
	325	330
Thr Gly Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr		
	340	345
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp		
	355	360

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 125  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.34

<400> 125

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Glu Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
  
 <210> 126  
 <211> 735  
 <212> PRT  
 <213> Unknown  
  
 <220>  
 <223> vp1, clone hu.36  
  
 <400> 126  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Ala Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 127  
 <211> 735  
 <212> PRT  
 <213> Unknown  
 <220>  
 <223> vp1, clone hu.45  
 <400> 127  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Pro Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Val Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 128  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.47

<400> 128

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Ser His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 129  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.13

<400> 129

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Gly Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
  
 <210> 130  
 <211> 735  
 <212> PRT  
 <213> Unknown  
  
 <220>  
 <223> vp1, clone hu.28  
  
 <400> 130  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Ser Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
370 375 380  
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
385 390 395 400  
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
405 410 415  
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
420 425 430  
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
435 440 445  
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
450 455 460  
Ala Gly Ala Ser Asp Ile Gln Asp Gln Ser Arg Asn Trp Leu Pro Gly  
465 470 475 480  
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
485 490 495  
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
500 505 510  
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
515 520 525  
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
530 535 540  
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
545 550 555 560  
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
565 570 575  
Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
580 585 590  
Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Gly Gln Asp  
595 600 605  
Arg Asp Val Tyr Leu Gln Gly Pro Thr Trp Ala Lys Ile Pro His Thr  
610 615 620  
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
625 630 635 640  
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655  
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670  
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685  
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
Page 197

690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 131  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.30

<400> 131

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270  
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285  
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300  
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320  
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
325 330 335  
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
340 345 350  
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
355 360 365  
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
370 375 380  
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
385 390 395 400  
Gln Met Leu Arg Thr Gly Asn Ser Phe Thr Phe Ser Tyr Thr Phe Glu  
405 410 415  
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
420 425 430  
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
435 440 445  
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
450 455 460  
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
465 470 475 480  
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
485 490 495  
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
500 505 510  
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
515 520 525  
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
530 535 540  
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
545 550 555 560  
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
565 570 575  
Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr



Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Gly Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 Page 201

465                      470                      475                      480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
                                  485                                   490                                   495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
                                  500                                   505                                   510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
                                  515                                   520                                   525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
                                  530                                   535                                   540  
 Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
                                  545                                   550                                   555                                   560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
                                  565                                   570                                   575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
                                  580                                   585                                   590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
                                  595                                   600                                   605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
                                  610                                   615                                   620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
                                  625                                   630                                   635                                   640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
                                  645                                   650                                   655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
                                  660                                   665                                   670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
                                  675                                   680                                   685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
                                  690                                   695                                   700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
                                  705                                   710                                   715                                   720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                                  725                                   730                                   735

<210> 133  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.19

<400> 133

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1                                   5                                   10                                   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
                                  20                                   25                                   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Glu Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp Tyr Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp

355	360	365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser 370 375 380		
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser 385 390 395 400		
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu 405 410 415		
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg 420 425 430		
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr 435 440 445		
Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln 450 455 460		
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly 465 470 475 480		
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn 485 490 495		
Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly 500 505 510		
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp 515 520 525		
Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys 530 535 540		
Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr 545 550 555 560		
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr 565 570 575		
Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr 580 585 590		
Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp 595 600 605		
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr 610 615 620		
Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys 625 630 635 640		
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn 645 650 655		
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln 660 665 670		
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys 675 680 685		

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 134  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.20

<400> 134

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Val  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Ala Ala Pro Gly Glu Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu

245	250	255
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr	260	265 270
Phe Gly Tyr Ser Thr Pro Trp Gly His Phe Asp Phe Asn Arg Phe His	275	280 285
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp	290	295 300
Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val	305	310 315 320
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu	325	330 335
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr	340	345 350
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp	355	360 365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser	370	375 380
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser	385	390 395 400
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu	405	410 415
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg	420	425 430
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr	435	440 445
Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln	450	455 460
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly	465	470 475 480
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn	485	490 495
Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly	500	505 510
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp	515	520 525
Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys	530	535 540
Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr	545	550 555 560
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr	565	570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Pro Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Ala Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 135  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.21

<400> 135

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 Page 207

130	135	140
Pro Val Glu His Ser 145	Pro Ala Glu Pro Asp 150	Ser Ser Ser Gly Thr Gly 155 160
Lys Ala Gly Gln Gln 165	Pro Ala Arg Lys Arg 170	Leu Asn Phe Gly Gln Thr 175
Gly Asp Ala Asp Ser Val 180	Pro Asp Pro Arg Pro 185	Leu Gly Gln Pro Pro 190
Ala Ala Pro Ser Gly Leu Gly 195	Thr Asn Thr Met Ala Ser 200 205	Gly Ser Gly
Ala Pro Met Ala Asp Asn 210	Asn Glu Gly Ala Asp Gly 215 220	Val Gly Asn Ser
Ser Gly Asn Trp His Cys 225	Asp Ser Thr Trp Met 230 235	Gly Asp Arg Val Ile 240
Thr Thr Ser Thr Arg 245	Thr Trp Ala Leu Pro 250	Thr Tyr Asn Asn His Leu 255
Tyr Lys Gln Ile Ser Ser 260	Gln Ser Gly Ala Ser 265	Asn Asp Asn His Tyr 270
Phe Gly Tyr Ser Thr Pro 275	Trp Gly Tyr Phe Asp 280	Phe Asn Arg Phe His 285
Cys His Phe Ser Pro Arg 290	Asp Trp Gln Arg Leu 295	Ile Asn Asn Asn Trp 300
Gly Phe Arg Pro Lys Arg 305	Leu Ser Phe Lys Leu 310 315	Phe Asn Ile Gln Val 320
Lys Glu Val Thr Gln 325	Asn Asp Gly Thr Thr 330	Thr Ile Ala Asn Asn Leu 335
Thr Ser Thr Val Gln 340	Val Phe Thr Asp Ser 345	Glu Tyr Gln Leu Pro Tyr 350
Val Leu Gly Ser Ala His 355	Gln Gly Cys Leu Pro Pro 360	Phe Pro Ala Asp 365
Val Phe Met Val Pro Gln 370	Tyr Gly Tyr Leu Thr 375	Leu Asn Asn Gly Ser 380
Gln Ala Val Gly Arg Ser 385	Ser Ser Phe Tyr Cys Leu 390 395	Glu Tyr Phe Pro Ser 400
Gln Met Leu Arg Thr 405	Gly Asn Asn Phe Thr 410	Phe Ser Tyr Thr Phe Glu 415
Asp Val Pro Phe His Ser 420	Ser Ser Tyr Ala His 425	Ser Gln Ser Leu Asp Arg 430
Leu Met Asn Pro Leu Ile 435	Asp Gln Tyr Leu Tyr Tyr 440	Leu Ser Arg Thr 445
Asn Thr Pro Ser Gly Thr 450	Thr Thr Met Ser Arg 455	Leu Gln Phe Ser Gln 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 136  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.24

<400> 136

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 Page 209

20					25					30					
Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			
Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				
Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80
Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
				85					90					95	
Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
			100						105					110	
Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Ile	Leu	Glu	Pro
		115					120					125			
Leu	Gly	Leu	Val	Glu	Glu	Pro	Val	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
	130					135					140				
Pro	Val	Glu	His	Ser	Pro	Ala	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Thr	Gly
145					150					155					160
Lys	Ala	Gly	Gln	Gln	Pro	Ala	Arg	Lys	Arg	Leu	Asn	Phe	Gly	Gln	Thr
				165					170					175	
Gly	Asp	Ala	Asp	Ser	Val	Pro	Asp	Pro	Arg	Pro	Leu	Gly	Gln	Pro	Pro
			180					185					190		
Ala	Ala	Pro	Ser	Gly	Leu	Gly	Thr	Asn	Thr	Met	Ala	Ser	Gly	Ser	Gly
		195					200					205			
Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ser
	210					215					220				
Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	Ile
225					230					235					240
Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	Leu
				245					250					255	
Tyr	Lys	Gln	Ile	Ser	Ser	Gln	Ser	Gly	Ala	Ser	Asn	Asp	Asn	His	Tyr
			260					265					270		
Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His
		275					280					285			
Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Asn	Trp
	290					295					300				
Gly	Phe	Arg	Pro	Lys	Arg	Leu	Ser	Phe	Lys	Leu	Phe	Asn	Ile	Gln	Val
305					310					315					320
Lys	Glu	Val	Thr	Gln	Asn	Asp	Gly	Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu
				325					330					335	
Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Ser	Glu	Tyr	Gln	Leu	Pro	Tyr
			340					345					350		

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
355 360 365  
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
370 375 380  
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
385 390 395 400  
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
405 410 415  
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
420 425 430  
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
435 440 445  
Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln  
450 455 460  
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
465 470 475 480  
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
485 490 495  
Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
500 505 510  
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
515 520 525  
Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
530 535 540  
Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
545 550 555 560  
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
565 570 575  
Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
580 585 590  
Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
595 600 605  
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
610 615 620  
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
625 630 635 640  
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655  
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670  
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 137  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.23-2

<400> 137

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Cys Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575

Gly Ser Val Ser Thr Tyr Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 138  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.22

<400> 138

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Gly Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Gly Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Thr Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln  
 450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
  
 <210> 139  
 <211> 735  
 <212> PRT  
 <213> Unknown  
  
 <220>  
 <223> vp1, clone hu.26  
  
 <400> 139  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 140  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.27

<400> 140

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Gly Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Val Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Val Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Ala Ala Thr Glu Gln Tyr  
 565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Val Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 141  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.4

<400> 141

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly 130 Leu Val Glu Glu Pro 135 Val Lys Thr Ala Pro 140 Gly Lys Lys Arg  
 Pro 145 Val Glu His Ser Pro 150 Val Glu Pro Asp Ser 155 Ser Ser Gly Thr Gly 160  
 Lys Ala Gly Gln Gln 165 Pro Ala Arg Lys Arg 170 Leu Asn Phe Gly Gln 175 Thr  
 Gly Asp Ala Asp 180 Ser Val Pro Asp Pro 185 Gln Pro Leu Gly Gln 190 Pro Pro  
 Ala Ala Pro 195 Ser Gly Leu Gly Ser 200 Thr Thr Met Ala Thr 205 Gly Ser Gly  
 Ala Pro 210 Met Ala Asp Asn Asn 215 Glu Gly Ala Asp Gly 220 Val Gly Asn Ser  
 Ser 225 Gly Asn Trp His Cys 230 Asp Ser Gln Trp Leu 235 Gly Asp Arg Val Ile 240  
 Thr Thr Ser Thr Arg 245 Thr Trp Ala Leu Pro 250 Thr Tyr Asn Asn His 255 Leu  
 Tyr Lys Gln Ile 260 Ser Ser Gln Ser Gly 265 Ala Ser Asn Asp Asn 270 His Tyr  
 Phe Gly Tyr 275 Ser Thr Pro Trp Gly 280 Tyr Phe Asp Phe Asn 285 Arg Phe His  
 Cys 290 His Phe Ser Pro Arg Asp 295 Trp Gln Arg Leu Val 300 Asn Asn Asn Arg  
 Gly 305 Phe Arg Pro Lys Arg 310 Leu Asn Phe Lys Leu 315 Phe Asn Ile Gln Val 320  
 Lys Glu Val Thr Gln 325 Asn Asp Gly Thr Thr 330 Thr Ile Ala Asn Asn 335 Leu  
 Thr Ser Thr Val 340 Gln Val Phe Thr Asp 345 Ser Glu Tyr Gln Leu 350 Pro Tyr  
 Val Leu Gly 355 Ser Ala His Gln Gly 360 Cys Leu Pro Pro Phe 365 Pro Ala Asp  
 Val 370 Phe Met Val Pro Gln Tyr 375 Gly Tyr Leu Thr Leu 380 Asn Asn Gly Ser  
 Gln 385 Ala Val Gly Arg Ser 390 Ser Phe Tyr Cys Leu 395 Glu Tyr Phe Pro Ser 400  
 Gln Met Leu Arg Thr 405 Gly Asn Asn Phe Gln 410 Phe Ser Tyr Thr Phe 415 Glu  
 Asp Val Pro Phe 420 His Ser Ser Tyr Ala 425 His Ser Gln Ser Leu 430 Asp Arg  
 Leu Met 435 Asn Pro Leu Ile Asp Gln 440 Tyr Leu Tyr Tyr Leu 445 Asn Lys Thr  
 Gln 450 Thr Asn Ser Gly Thr Leu 455 Gln Gln Ser Arg Leu 460 Leu Phe Ser Gln

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 142  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.5

<400> 142

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser Arg Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys

675                      680                      685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
     690                      695                      700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
     705                      710                      715                      720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                     725                      730                      735  
  
 <210> 143  
 <211> 735  
 <212> PRT  
 <213> Unknown  
  
 <220>  
 <223> vp1, clone hu.2  
  
 <400> 143  
 Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Thr Leu Ser  
     1                      5                      10                      15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
                     20                      25                      30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
                     35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
     50                      55                      60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
     65                      70                      75                      80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
                     85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
                     100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                     115                      120                      125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
     130                      135                      140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
     145                      150                      155                      160  
 Lys Ala Gly Gln Arg Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
                     165                      170                      175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
                     180                      185                      190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
                     195                      200                      205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
     210                      215                      220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
     225                      230                      235                      240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr



Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Gly Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 Page 229

450                      455                      460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465                      470                      475                      480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Gly Asn Asn  
                     485                      490                      495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
                     500                      505                      510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
                     515                      520                      525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
                     530                      535                      540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545                      550                      555                      560  
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr  
                     565                      570                      575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
                     580                      585                      590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
                     595                      600                      605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
                     610                      615                      620  
 Asp Gly His Phe His Pro Ser Pro Leu Thr Gly Gly Phe Gly Leu Lys  
 625                      630                      635                      640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
                     645                      650                      655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
                     660                      665                      670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
                     675                      680                      685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
                     690                      695                      700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705                      710                      715                      720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                     725                      730                      735

<210> 145  
 <211> 736  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.3

<400> 145

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1                      5                      10                      15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Arg Pro Gly Leu Arg Lys Pro Val Lys Thr Ala Pro Gly Lys Lys  
 130 135 140  
 Arg Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr  
 145 150 155 160  
 Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Asp Asp Arg Val  
 225 230 235 240  
 Ile Ala Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Cys Asn Asp Asn His  
 260 265 270  
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro  
 Page 231



Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val  
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 146  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.25

<400> 146

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Gly Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asn Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile

225	230	235	240
Thr Thr Ser Thr Arg 245	Thr Trp Ala Leu Pro 250	Thr Tyr Asn Asn His 255	Leu
Tyr Lys Gln Ile 260	Ser Ser Gln Ser Gly 265	Ala Ser Asn Asp Asn His 270	Tyr
Phe Gly Tyr 275	Ser Thr Pro Trp Gly 280	Tyr Phe Asp Phe Asn 285	Arg Phe His
Cys His 290	Phe Ser Pro Arg Asp 295	Trp Gln Arg Leu Ile 300	Asn Asn Asn Trp
Gly 305	Phe Arg Pro Lys Arg 310	Leu Asn Phe Lys Leu 315	Phe Asn Ile Gln Val 320
Lys Glu Val Thr 325	Gln Asn Asp Gly Thr Thr 330	Thr Thr Ile Ala Asn Asn 335	Leu
Thr Ser Thr Val 340	Gln Val Phe Thr Asp 345	Ser Glu Tyr Gln Leu 350	Pro Tyr
Val Leu Gly 355	Ser Ala His Gln Gly 360	Cys Leu Pro Pro Phe 365	Pro Ala Asp
Val Phe Met Val 370	Pro Gln Tyr Gly 375	Tyr Leu Thr Leu 380	Asn Asn Gly Ser
Gln Ala Val Gly Arg 385	Ser Pro Phe Tyr Cys 390	Leu Glu Tyr Phe Pro 395	Ser 400
Gln Met Leu Arg Thr 405	Gly Asn Asn Phe Gln 410	Phe Ser Tyr Thr Phe 415	Glu
Asp Val Pro Phe 420	His Ser Ser Tyr Ala 425	His Ser Gln Ser Leu 430	Asp Arg
Leu Met Asn 435	Pro Leu Ile Asp Gln 440	Tyr Leu Tyr Tyr Leu 445	Asn Lys Thr
Gln Thr Asn 450	Ser Gly Thr Leu 455	Gln Gln Ser Arg Leu 460	Leu Phe Ser Gln
Ala Gly Pro Thr Asn 465	Met Ser Leu Gln Ala 470	Lys Asn Trp Leu Pro 475	Gly 480
Pro Cys Tyr Arg Gln 485	Gln Arg Leu Ser Lys 490	Gln Ala Asn Asp Asn 495	Asn
Asn Ser Asn Phe 500	Pro Trp Thr Ala Ala 505	Thr Lys Tyr His Leu 510	Asn Gly
Arg Asp Ser 515	Leu Val Asn Pro Gly 520	Pro Ala Met Ala Ser 525	His Lys Asp
Asp Glu 530	Glu Lys Phe Phe Pro 535	Met His Gly Thr Leu 540	Ile Phe Gly Lys
Gln Gly Thr Asn Ala 545	Asn Asp Ala Asp Leu 550	Glu Asn Val Met Ile 555	Thr 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Asn Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 147  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.15  
 <400> 147

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro  
 50 55 60  
 Val Asp Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 Page 235

115	120	125
Leu Gly 130	Leu Val Gly Glu Pro 135	Val Lys Thr Ala Pro Gly Lys Lys Arg 140
Pro Val 145	Glu His Ser Pro 150	Val Glu Pro Asp Ser 155 Ser Ser Gly Thr Gly 160
Lys Ala Gly Asn 165	Gln Pro Ala Arg Lys 170	Arg Leu Asn Phe Gly Gln Thr 175
Gly Asp Ala Asp 180	Ser Val Pro Asp Pro 185	Gln Pro Leu Gly Gln Pro Pro 190
Ala Ala Pro 195	Ser Gly Leu Gly Ser 200	Thr Thr Met Ala Thr Gly Ser Gly 205
Ala Pro Val 210	Ala Asp Asn Asn 215	Glu Gly Ala Asp Gly Val Gly Asn Ser 220
Ser Gly 225	Asn Trp His Cys 230	Asp Ser Gln Trp Leu Gly Asp Arg Val Ile 240
Thr Thr Ser Thr 245	Arg Thr Trp Ala Leu Pro 250	Thr Tyr Asn Asn His Leu 255
Tyr Lys Gln 260	Ile Ser Ser Gln Ser 265	Gly Ala Ser Asn Asp Asn His Tyr 270
Phe Gly Tyr 275	Ser Thr Pro Trp Gly 280	Tyr Phe Asp Phe Asn Arg Phe His 285
Cys His 290	Phe Ser Pro Arg Asp 295	Arg Gln Arg Leu Ile Asn Asn Asn Trp 300
Gly Phe Arg Pro Lys 305	Arg Leu Asn Phe Lys 315	Leu Phe Asn Ile Gln Val 320
Lys Glu Val Thr 325	Gln Asn Asp Gly Thr 330	Thr Thr Ile Ala Asn Asn Leu 335
Thr Ser Thr Val 340	Gln Val Phe Thr Asp 345	Ser Gly Tyr Gln Leu Pro Tyr 350
Val Leu Gly 355	Leu Ala His Gln Gly 360	Cys Leu Pro Pro Phe Pro Ala Asp 365
Val Phe Met Val 370	Pro Gln Tyr Gly 375	Tyr Leu Thr Leu Asn Asn Gly Ser 380
Gln Ala Val Gly Arg 385	Ser Ser Phe Tyr Cys 390	Leu Glu Tyr Phe Pro Ser 400
Gln Met Leu Arg Thr 405	Gly Asn Asn Phe Gln 410	Phe Ser Tyr Thr Phe Glu 415
Asp Val Pro Phe 420	His Ser Ser Tyr Ala 425	His Ser Gln Ser Leu Asp Arg 430
Leu Met Asn 435	Pro Leu Ile Asp Gln 440	Tyr Leu Tyr Tyr Leu Asn Lys Thr 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asp Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Pro Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 148  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.16

<400> 148

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 Page 237

1	5	10	15
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro	20	25	30
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro	35	40	45
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro	50	55	60
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp	65	70	75
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala	85	90	95
Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly	100	105	110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro	115	120	125
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg	130	135	140
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly	145	150	155
Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr	165	170	175
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro	180	185	190
Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly	195	200	205
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser	210	215	220
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile	225	230	235
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu	245	250	255
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr	260	265	270
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His	275	280	285
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp	290	295	300
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val	305	310	315
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu	325	330	335

Thr Ser Thr Val<sub>340</sub> Gln Val Phe Thr Asp<sub>345</sub> Ser Glu Tyr Gln Leu<sub>350</sub> Pro Tyr  
 Val Leu Gly<sub>355</sub> Ser Ala His Gln Gly<sub>360</sub> Cys Leu Pro Pro Phe<sub>365</sub> Pro Ala Asp  
 Val Phe Met Val Pro Gln Tyr<sub>375</sub> Gly Tyr Leu Thr Leu<sub>380</sub> Asn Asn Gly Ser  
 Gln Ala Val Gly Arg Ser<sub>390</sub> Ser Phe Tyr Cys Leu<sub>395</sub> Glu Tyr Phe Pro Ser  
 Gln Met Leu Arg Thr<sub>405</sub> Gly Asn Asn Phe Gln<sub>410</sub> Phe Ser Tyr Thr Phe<sub>415</sub> Glu  
 Asp Val Pro Phe<sub>420</sub> His Ser Ser Tyr Ala<sub>425</sub> His Ser Gln Ser Leu<sub>430</sub> Asp Arg  
 Leu Met Asn<sub>435</sub> Pro Leu Ile Asp Gln<sub>440</sub> Tyr Leu Tyr Tyr Leu<sub>445</sub> Asn Lys Thr  
 Gln Ser Asn Ser Gly Thr Leu<sub>455</sub> Gln Gln Ser Arg Leu<sub>460</sub> Leu Phe Ser Gln  
 Ala Gly Pro Thr Ser Met<sub>470</sub> Ser Leu Gln Ala Lys<sub>475</sub> Asn Trp Leu Pro Gly<sub>480</sub>  
 Pro Cys Tyr Arg Gln<sub>485</sub> Gln Arg Leu Ser Lys<sub>490</sub> Gln Ala Asn Asp Asn<sub>495</sub> Asn  
 Asn Ser Asn Phe<sub>500</sub> Pro Trp Thr Ala Ala<sub>505</sub> Thr Lys Tyr His Leu<sub>510</sub> Asn Gly  
 Arg Asp Ser<sub>515</sub> Leu Val Asn Pro Gly<sub>520</sub> Pro Ala Met Ala Ser<sub>525</sub> His Lys Asp  
 Asp Glu Glu Lys Phe Phe Pro<sub>535</sub> Met His Gly Thr Leu<sub>540</sub> Ile Phe Gly Lys  
 Gln Gly Thr Asn Ala Asn<sub>550</sub> Asp Ala Asp Leu Asp<sub>555</sub> Asn Val Met Ile Thr<sub>560</sub>  
 Asp Glu Glu Glu Ile<sub>565</sub> Arg Thr Thr Asn Pro<sub>570</sub> Val Ala Thr Glu Gln<sub>575</sub> Tyr  
 Gly Tyr Val Ser<sub>580</sub> Asn Asn Leu Gln Asp<sub>585</sub> Ser Asn Thr Gly Pro<sub>590</sub> Thr Thr  
 Gly Thr Val<sub>595</sub> Asn His Gln Gly Ala<sub>600</sub> Leu Pro Gly Met Val<sub>605</sub> Trp Gln Asp  
 Arg Asp Val Tyr Leu Gln Gly<sub>615</sub> Pro Ile Trp Ala Lys<sub>620</sub> Ile Pro His Thr  
 Asp Gly His Phe His Pro<sub>630</sub> Ser Pro Leu Met Gly<sub>635</sub> Gly Phe Gly Leu Lys<sub>640</sub>  
 His Pro Pro Pro Gln<sub>645</sub> Ile Met Ile Lys Asn<sub>650</sub> Thr Pro Val Pro Ala<sub>655</sub> Asn  
 Pro Pro Thr Asn<sub>660</sub> Phe Ser Ser Ala Lys<sub>665</sub> Phe Ala Ser Phe Ile<sub>670</sub> Thr Gln

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 149  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.18

<400> 149

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Glu Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Ser Gly Ser Gly  
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Leu Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ser Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg Asn Leu  
 725 730 735

<210> 150  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.7

<400> 150

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Gly Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 151  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.8  
 <400> 151

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Thr Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 152  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone rh.56

<400> 152

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Gln Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Ala Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Arg Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 153  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.11

<400> 153

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr Arg Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 154  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.12

<400> 154

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Pro Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln

660                      665                      670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
           675                      680                      685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
           690                      695                      700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
           705                      710                      715                      720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                           725                      730                      735

<210> 155  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.9

<400> 155

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1                      5                      10                      15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
                           20                      25                      30  
 Lys Pro Ala Glu Arg His Gln Asp Asn Ser Arg Gly Leu Val Leu Pro  
                           35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Ser Asn Gly Leu Asp Lys Gly Glu Pro  
                           50                      55                      60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
                           85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
                           100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                           115                      120                      125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
                           130                      135                      140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145                      150                      155                      160  
 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
                           165                      170                      175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
                           180                      185                      190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
                           195                      200                      205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
                           210                      215                      220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Cys Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Pro Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr  
 Page 255

545                      550                      555                      560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
                                  565                                   570                                   575  
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
                                  580                                   585                                   590  
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
                                  595                                   600                                   605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
                                  610                                   615                                   620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
                                  625                                   630                                   635                                   640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
                                  645                                   650                                   655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
                                  660                                   665                                   670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
                                  675                                   680                                   685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
                                  690                                   695                                   700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
                                  705                                   710                                   715                                   720  
 Ser Glu Pro Cys Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                                  725                                   730                                   735

<210> 156  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.10  
 <400> 156

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1                                   5                                   10                                   15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
                                  20                                   25                                   30  
 Lys Leu Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro  
                                  35                                   40                                   45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                                  50                                   55                                   60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                                   70                                   75                                   80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
                                  85                                   90                                   95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
                                  100                                   105                                   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Leu Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445 450 455 460 465 470 475 480 485 490 495

435                      440                      445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
     450                      455                      460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
     465                      470                      475                      480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
                     485                      490                      495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
                     500                      505                      510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
                     515                      520                      525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
                     530                      535                      540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr  
     545                      550                      555                      560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
                     565                      570                      575  
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
                     580                      585                      590  
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
                     595                      600                      605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
     610                      615                      620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
     625                      630                      635                      640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
                     645                      650                      655  
 Pro Pro Thr Asn Tyr Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
                     660                      665                      670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Arg Lys  
     675                      680                      685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
     690                      695                      700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
     705                      710                      715                      720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                     725                      730                      735

<210> 157  
 <211> 736  
 <212> PRT  
 <213> Unknown  
 <220>  
 <223> vp1, clone hu.48

<400> 157

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
145 150 155 160  
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175  
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
180 185 190  
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
195 200 205  
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
210 215 220  
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
225 230 235 240  
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255  
Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His  
260 265 270  
Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
275 280 285  
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
290 295 300  
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
305 310 315 320  
Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn



Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
725 730 735

<210> 158  
<211> 736  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.44

<400> 158

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Glu Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly  
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala

210	215	220
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile 225 230 235 240		
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 245 250 255		
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His 260 265 270		
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe 275 280 285		
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn 290 295 300		
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln 305 310 315 320		
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn 325 330 335		
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 340 345 350		
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 355 360 365		
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly 370 375 380		
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro 385 390 395 400		
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe 405 410 415		
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp 420 425 430		
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg 435 440 445		
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser 450 455 460		
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro 465 470 475 480		
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn 485 490 495		
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn 500 505 510		
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys 515 520 525		
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly 530 535 540		

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575  
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590  
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720  
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735

<210> 159  
 <211> 736  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.46

<400> 159

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 Page 263



Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser  
 450 455 460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
 530 535 540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575  
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590  
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Ala Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720  
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735

<210> 160  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.43

<400> 160

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Pro Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
210 215 220  
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn  
260 265 270  
His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
275 280 285  
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
290 295 300  
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Val Gln Tyr Leu Tyr Tyr Leu Asn  
 435 440 445  
 Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe  
 450 455 460  
 Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu  
 465 470 475 480  
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp  
 485 490 495  
 Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu  
 500 505 510  
 Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His  
 515 520 525  
 Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe  
 530 535 540  
 Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met  
 545 550 555 560  
 Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro  
 580 585 590  
 Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile  
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser  
690 695 700

Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly  
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro  
725 730 735

Leu

<210> 161  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.38

<400> 161

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Cys His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 162  
 <211> 736  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.71

<400> 162

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
145 150 155 160  
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175  
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
180 185 190  
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
195 200 205  
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
210 215 220  
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
225 230 235 240  
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255  
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
260 265 270  
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
275 280 285  
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
290 295 300  
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
305 310 315 320  
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
325 330 335  
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
340 345 350  
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365  
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
370 375 380  
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser  
 450 455 460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505 510  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
 530 535 540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575  
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590  
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720  
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735

<210> 163  
 <211> 736  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone rh.43

<400> 163

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160  
 Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn  
 260 265 270  
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser  
 435 440 445  
 Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe  
 450 455 460  
 Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu  
 465 470 475 480  
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln  
 485 490 495  
 Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu  
 500 505 510  
 Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His  
 515 520 525  
 Lys Asp Asp Glu Glu Arg Phe Phe Pro Val Thr Gly Ser Cys Phe Trp  
 530 535 540  
 Gln Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu  
 545 550 555 560  
 Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu  
 565 570 575  
 Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln  
 580 585 590  
 Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr  
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val  
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 164  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.35

<400> 164

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 165  
 <211> 3161  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.136.1

<400> 165  
 gattgaattt agcgccgcg aattcgccct tgctgctca actggaccaa tgagaacttt 60  
 ccattcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc 120  
 aaggtcatgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa 180  
 tgtaagtcct cggcccagat agaccgact cccgtgattg tcacctcaa caccaacatg 240  
 tgcgccgtga ttgacgggaa ctcaacgacc ttcgagcacc agcagccgtt gcaagaccgg 300  
 atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag 360  
 gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420  
 tacgtcaaaa aggttgagc caagaaaaga cccgccccca gtgacgcaga tataagtga 480

cccaaacggg	cgcgcgggtc	agttgcgcag	ccatcgacgt	cagacgcgga	agcttcgatc	540
aactacgagg	acaggtacca	aaacaaatgt	tctcgtcacg	tgggcatgaa	tctgatgctg	600
tttccctgca	gacaatgcga	gagaatgaat	caaaattcaa	atatctgctt	cactcacgga	660
cagaaggact	gtttagagtg	ctttcccggtg	tcagaatctc	aaccgcgttc	tgtcgtcaaa	720
aaggcgatc	agaaactttg	ctacattcat	catatcatgg	gaaagggtgcc	agacgcttgc	780
actgcctgag	atctgggtcaa	tgtggatttg	gatgactgca	tctctgaaca	ataaatgatt	840
taaatcaggt	atggctgccc	atggttatct	tccagattgg	ctcaaggaca	ctctctctga	900
aggaataaga	cagtgggtgga	agctcaaacc	tggcccacca	ccaccaaagc	ccgcagagcg	960
gcataaggac	gacagcgggg	gtcttctgct	tcttgggtac	aagtacctcg	gaccttcaa	1020
cggactcgac	aaggagagcg	cgggtcaacga	ggcagacgcc	gcggccctcg	agtacgaca	1080
ggcctacgac	cggcagctcg	acagcggaga	caaccgtac	ctcaagtaca	accacgccga	1140
cgcgaggttt	caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	1200
agtcttccag	gcgaaaaaga	gggttcttga	acctctgggc	ctggttgagg	aacctgttaa	1260
gacggctccg	ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctctc	1320
gggaacagga	aaagcgggcc	agcagcctgc	gagaaagaga	ttgaattttg	gtcagactgg	1380
agacgcagac	tccgtacctg	accccagcc	tctcggacag	ccaccagcag	ccccctctgg	1440
tctgggaact	aatacgatgg	ctacaggcag	tggcgacca	atggcagaca	ataacgaggg	1500
cgccgacgga	gtgggtaatt	cctcgggaag	ttggcattgc	gattccacat	ggatgggcga	1560
cagagtcac	accaccagca	cccgaacctg	ggctctgccc	acctacaaca	accatctgta	1620
caagcagatc	tccagccaat	caggagccag	caacgacaac	cactactttg	gctacagcac	1680
cccttggggg	tattttgact	tcaacagatt	ccactgccac	ttttcaccac	gtgactggca	1740
aagactcatc	aacaacaact	ggggattccg	gcccgaagaga	ctcaacttca	agctctttaa	1800
cattcaagtc	aaggaggtca	cgcagaatga	cggtagcagc	acgattgcca	ataaccttac	1860
cagcacgggt	cagggtgtta	ctgactcgga	gtaccagctc	ccgtacgtcc	ccggctcggc	1920
gcatacaagg	tgcttcccgc	cgttcccagc	agacgtcttc	atgggtgccac	agtatggata	1980
cctcacccctg	aacaacggga	gtcaggcagt	aggacgctct	tcattttact	gcctggagta	2040
ctttccttct	cagatgcttc	gtaccggaaa	caactttacc	ttcagctaca	cctttgagga	2100
tgttcctttc	cacagcagct	acgctcacag	ccagagtgtg	gaccgtctca	tgaatcctct	2160
catcgaccag	tacctgtatt	acttgagcag	aacaacact	ccaagcggaa	ccaccacgca	2220
gtccaggcct	cagttttctc	aggccggagc	aagtgcattt	cgggaccagt	ctaggaactg	2280
gcttcctgga	ccctgttacc	gccagcagcg	agtatcaaag	acagctgcgg	acaacaacaa	2340
cagtgaatac	tcgtggactg	gagctaccaa	gtaccacctc	aatggcagag	actctctggt	2400
gaatccgggc	ccggccatgg	ccagccacaa	ggacgatgaa	gaaaagtttt	ttcctcaaag	2460
cggggttctc	atctttggga	agcaaggctc	agagaaaaca	aatgtggaca	ttgaaaaggt	2520
catgattaca	gacgaagagg	aaatcagaac	caccaatccc	gtggccacgg	agcagtatgg	2580
ttctgtatct	accaacctcc	agagcggcaa	cacacaagca	gctactgcag	atgtcaacac	2640
acaaggcggt	cttccaggca	tggcttgcca	ggacagagac	gtgcacctgc	aggggcctat	2700
ctgggcaaa	attccacaca	cggacggaca	ttttcacccc	tctcccctca	tgggcggatt	2760
tggacttaaa	caccctctc	cacagattct	catcaagaac	accccggtac	ctgcaaattc	2820
ttcgaccacc	ttcagtgcgg	caaagtgtgc	ttccttcac	acacagtatt	ccacagggca	2880
ggtcagcgtg	gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaaccccga	2940
gatccagtac	acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	tggacactaa	3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt	3060
gcttgtaaat caataaacg ttttaattcgt ttcagttgaa ctttggtctc tgccaagggc	3120
gaattcgttt aaaccttgca ggactagtcc ctttagtgag g	3161

<210> 166  
 <211> 3162  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.140.1

<400> 166	
gaattgaatt tagcgccgc gaattcgccc ttcgcagaga ccaaagtca actgaaacga	60
attaaacggt ttattgatta acaagcaatt acagattacg agtcaggat ctggtgcaa	120
tggggcgagg ctctgaatac acgccattag tgtccacagt aaagtccaca ttaacagact	180
tggtgtgatt ggaagtgtac tgaatttcgg gattccagcg tttgctgtt tccttctgca	240
gctccactc gatctccacg ctgacctgtc ccgtggagta ctgtgtgatg aaggaagcaa	300
actttgccgc actgaagggt gtcgaaggat tcgcaggatc cgggggtgtt ttgatgagaa	360
tctgtggagg aggggtgtta agtccgaatc caccatgag gggagagggg tgaaaatgtc	420
cgtccgtgtg tggaatcttt gccagatgg gccctgaag gtacacatct ctgtcctgcc	480
agaccatgcc tggaagaacg ccttgtgtgt tgacatctgc ggtagctgct tgtctgttgc	540
ctctctggag gttggttagat acagaaccgt actgctccgt agccacggga ttggtgttcc	600
tgatttcctc ttcgtctgta atcatgacct tttcaatgtc cacattgtt ttctctgagc	660
cttgcttccc aaagatgaga accccgctct gaggaaaaaa cttttcttca ttgtccttgt	720
ggcttgccat ggccgggccc ggattcacca gagagtctct gccattgagg tggacttgg	780
tagctccagt ccacgagtat tcaactgtgt tggtatccgc agatgtctt gatactcgt	840
gctggcggta acaggggtcca ggaagccagt tcctagactg gtcccgaatg tcaactcgtc	900
cggcctgaga aaactgaagc cttgactgcg tgggtgttcc acttgagtg tttgtgtg	960
tcaagtaata caggtagtgg tcgatgagag gattcatgag acggtccaga ctctggctgt	1020
gagcgtagcc gctgtggaag ggaacgtcct caaaagtgt gctgaaggta aagttgtt	1080
cggtagcgag catctgagaa ggaaagtact ccaggcagta aaatgaagag cgtcctactg	1140
cctgactccc gttgttcagg gtgaggtatc catactgtgg caccatgaag acgtctgtg	1200
ggaacggcgg gaggcatcct tgatgcgccc agccgaggac gtacgggagc tggtagtccg	1260
agtcagtaaa cacctgaacc gtgctggtaa ggttattggc aatcgtcgtc gtaccgtcat	1320
tctgcgtgac ctctttgact tgaatgttaa agagcttgaa gttgagtctc ttgggtcgga	1380
atccccagtt gttgttgatg agtctttgcc agtcacgtgg tgaaaagtgg cagtggatc	1440
tggtgaagtc aaaatacccc caaggggtgc tgtagccaaa gtagtgattg tcgttcgagg	1500
ctcctgattg gctggaaatt tgttttaga ggtggtgtt gtaggtggg agggcccagg	1560
ttcgggtgct ggtggtgatg actctgtcgc ccatccatgt ggaatcgcaa tgccaatttc	1620
ccgaggaatt acccactccg tcggcgccct cgttattgtc tgccattggt gcgccactgc	1680
ctgtagccat cgtattagtt cccagaccag agggggctgc tgggtggctgt ccgagaggct	1740
gggggtcagg tactgagtct gcgtctccag tctgaccaa attcaatctt tttcttgag	1800
gctgctggcc cgcttttccg gttcccagg aggagtctgg ctccacagga gagtgtcta	1860
ccggcctctt ttttcctgga gccgtcttga caggttcccc aaccaggccc agaggttcaa	1920
gaaccctctt tttcgcctgg aagactgctc gtccgagggt gcccccaaaa gacgtatctt	1980

ctttaaggcg	ctcctgaaac	tccgcgtcgg	cgtggttgta	cttgaggtag	gggttgcttc	2040
cgctgtcgag	ctgccgggtcg	taggcctttgt	cgtgctcgag	ggccgcggcg	tctgcctcgt	2100
tgaccggctc	tcccttgctg	agtccgttga	aggggtccgag	gtacttgtag	ccaggaagca	2160
caagaccctt	gctgtcgtcc	ttatgccgct	ctgcgggctt	tggtggtggt	gggccagggt	2220
tgagcttcca	ccactgtctt	attccttcag	agagagtgtc	ctcgagccaa	tctggaagat	2280
aaccatcggc	agccatacct	gatttaaatc	atttattgtt	caaagatgca	gtcatccaaa	2340
tccacattga	ccagatcgca	ggcagtgcga	gcgtctggca	cctttcccat	gatatgatga	2400
atgtagcaca	gtttctgata	cgcctttttg	acgacagaaa	cgggttgaga	ttctgacacg	2460
ggaaagcact	ctaaacagtc	tttctgtccg	tgagtgaagc	agatatttga	attctgattc	2520
attctctcgc	attgtctgca	gggaaacagc	atcagattca	tgcccacgtg	acgagaacat	2580
ttgttttggt	acctgtctgc	gtagtgtatc	gaagcttccg	cgtctgacgt	cgatggctgc	2640
gcaactgact	cgcgcacccg	tttgggtctc	cttatatctg	cgtcactggg	ggcgggtctt	2700
ttcttggtc	cacccttttt	gacgtagaat	tcatgctcca	cctcaaccac	gtgatccttt	2760
gcccaccgga	aaaagtcttt	gacttcctgc	ttggtgacct	tcccaaagtc	atgatccaga	2820
cggcgggtga	gttcaaattt	gaacatccgg	tcttgcaacg	gctgctggtg	ttcgaaggtc	2880
gttgagttcc	cgtcaatcac	ggcgacatg	ttggtgttgg	aggtgacgat	cacgggagtc	2940
gggtctatct	gggccgagga	cttgcatctt	tggtccacgc	gcaccttgct	tcctccgaga	3000
atggctttgg	ccgactccac	gacctggcg	gtcatcttcc	cctcctccca	ccagatcacc	3060
atcttgtcga	cacagtcggt	gaagggaaag	ttctcattgg	tccagttgac	gcagcaaggg	3120
cgaattcggt	taaacctgca	ggactagtcc	ctttagttag	gg		3162

<210> 167  
 <211> 3164  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.140.2

<400> 167	
gcgaattgaa	tttagcggcc
gcgaattcgc	ccttcgcaga
gaccaaagtt	caactgaaac
gaattaaacg	gtttattgat
taacaagcaa	ttacaaatta
cgagtcagg	atctggtgcc
aatggggcga	ggctctgaat
acacgccatt	agtgtccaca
gtaaagtcca	cattaacaga
cttggttag	ttggaagtgt
actgaatttc	gggattccag
cgtttgctgt	tttccttctg
cagctccac	tcgatctcca
cgctgacctg	tcccgtggag
tactgtgtga	tgaaggagc
aaactttgcc	gactgaagg
tggtcgaagg	attcgcagg
accgggggtg	tcttgatgag
aatctgtgga	ggagggtgtt
taggtccgaa	tccacccatg
aggggagagg	ggtgaaaatg
tccgtccgtg	tggtgaatct
ttgccagat	gggcccttga
aggtacacat	ctctgtcctg
ccagaccatg	cctggaagaa
cgccttggtg	gttgacatct
gcggtagctg	cttgtctggt
gcctctctgg	aggttggttag
atacagaacc	atactgtctc
gtagccacgg	gattggttgt
cctgatttcc	tcttcgtctg
taatcatgac	cttttcaatg
tccacatttg	ttttctctga
gccttgcttc	ccaaagatga
gaaccccgct	ctgaggaaaa
aacttttctt	cattgtcctt
gtggcttgcc	atggccgggc
ccggattcac	cagagagtct
ctgccattga	ggtggtactt
ggtagctcca	gtccacgagt
attcactggt	gttggttatcc
gcagatgtct	ttgatactcg
ctgctggcgg	taacaggggtc
cagggaagcca	gttccttagac
tggtcccga	tgctactcgc
tccggcctga	gaaaactgaa
gccttgactg	cgtggtggtt
ccacttgag	tggttggtgt
gctcaagtaa	tacagggtact
ggtcgatgag	aggattcatg
agacgggtcca	gactctggct

gtgagcgtag	ctgctgtgga	aaggaacgtc	ctcaaaagt	tagctgaagg	taaagttggt	1080
tccggtacgc	agcatctgag	aaggaaagta	ctccgggcag	taaaatgaag	agcgtcctac	1140
tgcctgactc	ccgttgctca	gggtgaggta	tccatactgt	ggcaccatga	agacgtctgc	1200
tgggaacggc	gggaggcatc	cttgatgcgc	cgagccgagg	acgtacggga	gctggtactc	1260
cgagtcagta	aacacctgaa	ccgtgctggt	aaggttattg	gcaatcgtcg	tcgtaccgtc	1320
attctgcgtg	acctctttga	cttgaatggt	aaagagcttg	aagttgagtc	tcttgggtcg	1380
gaatccccag	ttgttggtga	tgagtctttg	ccagtcacgt	ggtgaaaagt	ggcagtgga	1440
tctgttgaag	tcaaaatacc	cccaaggggt	gctgtagcca	aagtagtgat	tgctgttcga	1500
ggctcctgat	tggctggaaa	tttgtctgta	gaggtggttg	ttgtaggtgg	gcagggccca	1560
ggttcgggtg	ctgggtggtg	tgactctgtc	gcccattccat	gtggaatcgc	aatgccgatt	1620
tcccaggaa	ttaccactc	cgtcggcgcc	ctcgttattg	tctgccattg	gtgcgccact	1680
gcctgtagcc	atcgtattag	ttcccagacc	agagggggct	gctggtggct	gtccgagagg	1740
ctgggggtca	ggtactgagt	ctgcgtctcc	agtctgacca	aaattcaatc	tttttcttgc	1800
aggctgctgg	cccgcctttc	cggttcccga	ggaggagtct	ggctccacag	gagagtgtct	1860
taccggcctc	ttttttcccg	gagccgtctt	aacaggttcc	ccaaccaggc	ccagaggttc	1920
aagaaccctc	tttttcgcct	ggaagactgc	tcgtccgagg	ttgcccccaa	aagacgtatc	1980
ttctttaagg	cgctcctgaa	actccgcgtc	ggcgtggttg	tacttgaggt	acgggttgtc	2040
tccgctgtcg	agctgccggg	cgtaggcttt	gtcgtgctcg	agggccgcgg	cgtctgcctc	2100
gttgaccggc	tctcccttgt	cgagtccggt	gaaggggtccg	aggtacttgt	acccagggaag	2160
cacaagacc	ctgctgtcgt	ccttatgccg	ctctgcgggc	tttgggtggtg	gtgggcccagg	2220
tttgagcttc	caccactgtc	ttattccttc	agagagagtg	tcctcgagcc	aatctggaag	2280
ataaccatcg	gcagccatac	ctgatttaaa	tcattttattg	ttcaaagatg	cagtcatcca	2340
aatccacatt	gaccagatcg	caggcagtgc	aagcgtcttg	cacctttccc	atgatatgat	2400
gaatgtagca	cagtttctga	tacgcctttt	tgacgacaga	aacgggttga	gattctgaca	2460
cgggaaagca	ctctaacag	tctttctgtc	cgtagagtga	gcagatattt	gaattctgat	2520
tcattctctc	gcattgtctg	cagggaaaca	gcatcagatt	catgcccacg	tgacgagaac	2580
atttgttttg	gtacctgtct	gcgtagtgtg	tcgaagcttc	cgcgtctgac	gtcgatggct	2640
gcgcaactga	ctcgcgcacc	cgtttggggc	cacttatatc	tgcgctactg	ggggcgggtc	2700
ttttcttggc	tccacccttt	ttgacgtaga	attcatgtct	cacctcaacc	acgtgatcct	2760
ttgcccaccg	gaaaaagtct	ttgacttcct	gcttggtgac	cttcccaaag	tcatgatcca	2820
gacggcgggt	gagttcaa	ttgaacatcc	ggtcttgcaa	cggctgctgg	tggtcgaagg	2880
tcgttgagtt	cccgtcaatc	acggcgcaca	tggtggtggt	ggaggtgacg	atcacgggag	2940
tcgggtctat	ctgggcccag	gacttgcatt	tctggtccac	gcgcaccttg	cttcctccga	3000
gaatggcttt	ggccgactcc	acgaccttgg	cggtcattct	cccctcctcc	caccagatca	3060
ccatcttgtc	gacacagtcg	ttgaaggga	agttctcatt	ggtccagttg	acgcagcaag	3120
ggcgaattcg	tttaaacctg	caggactagt	cccttttagtg	aggg		3164

<210> 168  
 <211> 3159  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.147.2

<400> 168

gattgattta	gcggcccgca	attcgccctt	gctgctcaa	ctggaccaat	gagaactttc	60
ccttcaacga	ttgcgtcgac	aagatggtga	tctggtggga	ggagggaaaag	atgaccgcca	120
aggctcgtga	gtcggccaaa	gccattctcg	gaggaagcaa	ggtgctgtg	gaccaaagt	180
gcaagtcttc	ggcccagatc	gacccgactc	ccgtgatcgt	cacctccaac	accaacatgt	240
gcgccgtgat	tgatggaaac	tcaacgacct	tcgagcacca	gcagccgttg	caagaccgga	300
tgttcaaatt	tgaacttacc	cgccgtctgg	atcatgactt	tggaaaggtc	accaagcagg	360
aagtgaaga	ctttttccgg	tgggcaaagg	atcacgtggt	tgaggaggag	catgagttct	420
acgtcaaaaa	gggtggagcc	aaaaaaagac	ccgccccag	tgacgcagat	ataagtgagc	480
ccaaacgggc	gcgcgagtca	gttgccgagc	catcgacgtc	agacgcggaa	gcttcgatca	540
actacgcgga	caggtaccaa	aacaaatggt	ctcgtcacgt	gggcatgaat	ctgatgctgt	600
ttccctgcag	acaatgcgag	agaatgaatc	agaattcaaa	tatctgcttc	actcacggac	660
agaaagactg	tccatagtg	tttcccgtgt	cagaatctca	acccgtttct	gtcgtcaaaa	720
aggcgtatca	gaaactgtgc	tacattcatc	acatcatggg	aaagggtgcca	gacgcttgca	780
ctgcttgcca	cctggtcaat	gtggatttgg	atgactgcat	ctctgaacaa	taaatgattt	840
aaatcaggta	tggctgccga	tggttatctt	ccagattggc	tcgaggacac	tctctctgaa	900
ggaataagac	agtggaggaa	gctcaaacct	ggcccaccac	caccaaagcc	cgagagcgg	960
cataaggacg	acagcagggg	tcttgtgctt	cctggatata	agtacctcgg	acccttcaac	1020
ggactcgaca	agggagagcc	ggtcaacgag	gcagacgccc	cggccctcga	gcacgacaag	1080
gcctacgacc	ggcagctcga	cagcggagac	aacccgtacc	tcaagtacaa	ccacgccgac	1140
gcggagtttc	aggagcgctt	taaagaagat	acgtcttttg	ggggcaacct	cggacgagca	1200
gtcttccagg	cgaaaaagag	ggttcttgaa	cctctggggc	tggttgagga	acctgttaag	1260
acggctccgg	gaaaaaagag	gccggtagag	cactctctctg	tggagccaga	ctcctctctg	1320
ggaaccggaa	aagcgggcaa	ccagcctgca	agaaaaagat	tgaatttcgg	tcagactgga	1380
gacgcagact	ccgtacctga	cccccagcct	ctcggacagc	caccagcatc	cccctctggt	1440
ctgggaacta	atacgatggc	tacaggcagt	ggcgcaccaa	tggcagacaa	taacgagggc	1500
gccgacggag	tgggtaattc	ctcgggaaat	tggcattgag	attccacatg	gatgggcgac	1560
agagtcgtca	ccaccagcac	ccgcacctgg	gccctgcccc	cctacaacaa	ccacctctac	1620
aagcagattt	ccagccaatc	aggagccagc	aacgacaacc	actactttgg	ctacagcacc	1680
ccttgggggt	attttgactt	caacagattc	cactgccaact	tttcgccacg	cgactggcag	1740
agactcatca	acaacaactg	gggattccgg	cccaaaagac	tcaacttcaa	gctgtttaac	1800
attcaagtca	aggagggtcac	gcagaatgac	ggtacgacga	cgattgccaa	taaccttacc	1860
agcacggttc	agggtgtttac	tgacttggag	taccagctcc	cgtacgtcct	cggctcggcg	1920
catcaaggat	gcctcccggc	gttcccagca	gacgtcttca	tggtgccaca	gtatggatac	1980
ctcaccctga	acaacgggag	tcaggcggta	ggacgctctt	ccttttactg	cctggagtac	2040
tttcttcttc	agatgcttcg	caccggaaac	aactttacct	tcagctacac	ttttgaagac	2100
gttcctttcc	acagcagcta	cgctcacagt	caaagtctgg	accgtctcat	gaatcctctc	2160
atcgaccagt	acctgtatta	cttgagcaga	acaaacactc	caagcggaac	cactacgcag	2220
tccaggcttc	agttttctca	ggccggagcg	agtgcatttc	gggaccagtc	taggaactgg	2280
cttcttgga	cctgttaccg	ccagcagcga	gtatcaaaga	cagctgcgga	taacaacaac	2340
agtgaatact	cgtggactgg	agctaccaag	taccacctca	atggcagaga	ctctctggtg	2400
aatccgggcc	cggccatggc	cagccacaag	gacgatgaag	aaaagttttt	tcctcaaagc	2460
ggggttctca	tctttgggaa	gcaaggctca	gagaaaacaa	atgtggacat	tgaaaaggtc	2520

atgattacag	acgaagagga	aatcaggacc	accaatcccc	tggctacgga	gcagtatggt	2580
tctgtatcta	ccaacctcca	gagcggcaac	acacaagcag	ctacctcaga	tgtcaacaca	2640
caaggcggtc	ttccaggcat	ggtctggcag	gacagagacg	tgtacctgca	ggggcccatc	2700
tgggcaaaaa	ttccacacac	ggacggacat	tttcacccct	ctccccctcat	gggcggattt	2760
ggacttaaac	accctcctcc	acagattctc	attaagaata	ccccggtacc	tgcaatcct	2820
tcgaccacct	tcagcgcggc	aaagtttgct	tccttcatca	cacagtattc	cacggggcag	2880
gtcagcgtgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaaacgctg	gaatcccga	2940
attcagtaca	cttccaacta	caacaaatct	gttaatgtgg	actttactgt	ggacactaat	3000
ggggtgtatt	cagagcctcg	ccctattggc	accagatacc	tgactcgtaa	tctgtaattg	3060
cttgtaaatc	aataaaccgt	ttaattcggt	tcagttgaac	tttggctctc	gcgaagggcg	3120
aattcgttta	aacctgcagg	actagtcctt	ttagtgagg			3159

<210> 169  
 <211> 3156  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.147.3

<400> 169						
cgattgaatt	tagcggccgc	gaattcgccc	ttgctgcgtc	aacggaccaa	tgagaacttt	60
cccttcaacg	attgctcgca	caagatgggtg	atctggtggg	aggagggaaa	gatgaccgcc	120
aaggctcgtg	agtcggccaa	agccattctc	ggaggaagca	aggtgcgtgt	ggaccaaag	180
tgcaagtctt	cgcccgagat	cgaccgact	cccgtgatcg	tcacctcaa	caccaacatg	240
tgcgccgtga	ttgatggaaa	ctcaacgacc	ttcgagcacc	agcagccgtt	gcaagaccgg	300
atgttcaaat	ttgaacttac	ccgccgtctg	gatcatgact	ttggaaagg	caccaagcag	360
gaagtgaag	actttttccg	gtgggcaaag	gatcacgtgg	ttgaggtgga	gcatgagttc	420
tacgtcaaaa	aggggtggagc	caaaaaaaga	cccgcccca	gtgacgcaga	tataagttag	480
cccaaaccgg	cgcgcgagtc	agttgcgcag	ccatcgacgt	cagacgcgga	agcttcgac	540
aactacgcgg	acaggtacca	aaacaaatgt	tctcgtcacg	tgggcatgaa	tctgatgctg	600
tttccttgca	gacaatgcga	gcgaatgaat	cagaattcaa	atatctgctt	cactcacgga	660
cagaaagact	gttttagagt	ctttcccgtg	tcagaatctc	aaccgctt	tgctgtcaaa	720
aaggcgtatc	agaaactgtg	ctacattcat	cacatcatgg	gaaagggtgc	agacgcttgc	780
actgcttgcg	acctgggtcaa	tgtggatttg	gatgactgca	tctctgaaca	ataaatgatt	840
taaatcaggt	atggctgccc	atggttatct	tccagattgg	ctcgaggaca	ctctctctga	900
aggaataaga	cagtgggtgga	agctcaaacc	tggccacca	ccaaagccc	cagagcggca	960
taaggacgac	agcaggggtc	ttgtgcttcc	tggatacaag	tacctcgga	ccttcaacgg	1020
actcgacaag	ggagagccgg	tcaacgaggc	agacgccg	gccctcgagc	acgacaaggc	1080
ctacgaccgg	cagctcgaca	gcggagacaa	cccgtacctc	aagtacaacc	acgccgacgc	1140
ggagtttcag	gagcgctta	aagaagatac	gtcttttggg	ggcaacctcg	gacgagcagt	1200
cttccaggcg	aaaaagaggg	ttcttgaacc	tctgggcctg	gttgaggaac	ctgttaagac	1260
ggctccggga	aaaaagaggc	ccgtagagca	ctctcctgtg	gagccagact	cctcctcggg	1320
aaccggaaaa	gcgggcaacc	agcctgcaag	aaaaagattg	aatttcgggtc	agactggaga	1380
cgcagactcc	gtacctgacc	cccagcctct	cggacagcca	ccagcagccc	cctctggtct	1440
gggaactaat	acgatggcta	caggcagtg	cgcaccaatg	gcagacaata	acgagggcgc	1500

cgacggagtg	ggtaattcct	cgggagattg	gcattgcat	tccacatgga	tgggcgacag	1560
agtcattcacc	accagcacc	gcacctgggc	cctgcccacc	tacaacaacc	acctctacaa	1620
gcagatttcc	agccaatcag	gagccagcaa	tgacaaccac	tactttggct	acagcacccc	1680
ttgggggtat	tttgacttca	acagattcca	ctgccacttt	tcgccacgcg	actggcagag	1740
actcatcaac	aacaactggg	gattccggcc	caaaagactc	aacctcaagc	tgtttaacat	1800
tcaagtcaag	gaggtcacgc	agaatgacgg	tacgacgacg	attgccaata	accttaccag	1860
cacggttcag	gtgtttactg	acttggagta	ccagctcccg	tacgtcctcg	gctcggcgca	1920
tcaaggatgc	ctcccgccgt	tcccagcaga	cgtcttcatg	gtgccacagt	atggatacct	1980
cacctgaac	aacgggagtc	aggcggtagg	acgctcttcc	ttttactgcc	tgaggtactt	2040
tccttctcag	atgcttcgta	ccggaaacaa	ctttaccttc	agctacactt	ttgaagacgt	2100
tcctttccac	agcagctacg	ctcacagtca	aagtctggac	cgtctcatga	atcctctcat	2160
cgaccagtac	ctgtattact	tgagcagaac	aaacactcca	agcggaaacca	ctacgcagtc	2220
caggcttcag	ttttctcagg	ccggagcgag	tgacattcgg	gaccagtcta	ggaactggct	2280
tcctggagcc	tgttaccgcc	agcagcgagt	atcaaagaca	gctgcggata	acaacaacgg	2340
tgaataactcg	tggaactggag	ctaccaagta	ccacctcaat	ggcagagact	ctctggtgaa	2400
tccggggccc	gccatggcca	gccacaagga	cgatgaagaa	aagttttttc	ctcaaagcgg	2460
ggttctcatc	tttgggaagc	aaggctcaga	gaaaacaaat	gtggacattg	aaaagggtcat	2520
gattacagac	gaagagggaaa	tcaggaccac	caatcccgtg	gctacggagc	agtatggttc	2580
tgtatctacc	aacctccaga	gcggcaacac	acgagcagct	acctcagatg	tcaacacaca	2640
aggcgttctt	ccaggcatgg	tctggcagga	cagagacgtg	tacctgcagg	ggcccatctg	2700
ggcaaaaatt	ccacacacgg	acggacattt	tcacccctct	cccctcatgg	gcggatttgg	2760
acttaaacac	cctcctccac	agatttctcat	taagaatacc	ccggtacctg	cgaatccttc	2820
gaccaccttc	agcgcggcaa	agtttgcttc	cttcatacaca	cagtattcca	cggggcaggt	2880
cagcgtggag	atcgagtggg	agctgcagaa	ggagaacagc	aaacgctgga	atcccgaat	2940
tcagtacact	tccaactaca	acaaatctgt	taatgtggac	tttactgtgg	acactaatgg	3000
ggtgtattca	gagcctcgcc	ctattggcac	cagatacctg	actcgtaatc	tgtaattgct	3060
tgtaaatcaa	taaaccgttt	aattcgtttc	agttgaactt	tggtctctgc	gaagggcgaa	3120
ttcgtttaaa	cctgcaggac	tagtcccttt	agtgag			3156

<210> 170  
 <211> 3158  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.161.10

<400>	170					
gattgaattt	agcggccgcg	aattcgccct	tgctgcgtca	actggaccaa	tgagaacttt	60
cctttcaatg	attgcgtcga	caagatggtg	atctggtggg	aggagggaaa	gatgaccgcc	120
aaggctcgtg	agtcggccaa	agccattctc	ggaggaagca	aggtgcgcgc	ggaccagaaa	180
tgcaagtcct	cggcccagat	agacccgact	cccgtgattg	tcacctccaa	caccaacatg	240
tgcgccgtga	ttgacgggaa	ctcaacgacc	ttcgaacacc	agcagccgtt	gcaagaccgg	300
atgttcaaat	ttgaactcac	ccgccgtctg	gatcatgact	ttgggaagg	caccaagcag	360
gaagtcaaa	actttttccg	gtgggcaaag	gatcacgtgg	ttgaggtgga	gcatgaattc	420
tacgtcaaaa	aggggtggag	taagaaaaga	cccgcacca	gtgacgcaga	tataagtga	480
cccaaacggg	cgcgcgagtc	agttgcgcag	ccatcgacgt	cagacgcgga	agcttcgatc	540

aactacg	cg	gcaggtacca	aaacaaatgt	tctcgtcacg	tgggcatgaa	tctgatgctg	600
tttcctt	gca	gacaatgcga	gagaatgaat	cagaattcaa	atatctgctt	cactcacgga	660
cagaaag	act	gttttagagt	ctttcccg	tg	cagaatctc	aaccgcttc	720
aaggcgt	tatc	agaaactttg	ctacattcat	catatcatgg	gaaagggtgcc	agacgcttgc	780
actgcct	g	atctgggtcaa	tgtggatttg	gatgactgca	tctctgaaca	ataaatgatt	840
taaatcag	gt	atggctg	ccg	atggttatct	tccagattgg	ctcgaggaca	900
aggaata	aga	cagtgggtgga	agctcaaacc	tggcccacca	ccaccaaagc	ccgcagagcg	960
gcataagg	ac	gacagcaggg	gtctt	gtgct	tcctgggtac	aagtacctcg	1020
cggactc	gac	aagggggagc	cgg	tcaacga	ggcagacgcc	gcggccctcg	1080
ggcctac	gac	cggcagctcg	acagcggaga	caaccctgac	ctcaagtaca	accacgccga	1140
cg	cggag	ttt	caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	1200
agtcttcc	ag	gcaaaaaaga	gggttcttga	acctctgggc	ctggttgagg	aacctgttaa	1260
aacggctcc	g	gaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	1320
gggaacc	gga	aaagcggg	cc	agcagcctgc	aagaaaaaga	ttgaatttcg	1380
agacgcag	ac	tccgtac	ctg	acccccagcc	tctcggacag	ccaccagcag	1440
tctggg	atct	actacaatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgagg	1500
tgccgat	gga	gtgggtaatt	cctcgggaaa	ttggcattgc	gattcccaat	ggctgggcga	1560
cagagtc	atc	accaccagca	ccgcac	ctg	ggccctgccc	acctacaaca	1620
caagcaa	atc	tccagccaat	caggagcctc	aaacgacaac	cactactttg	gctacagcac	1680
cccctg	gggg	tattttgact	tcaacagatt	ccactgccac	ttttcaccac	gtgactggca	1740
aagactc	atc	aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttaa	1800
cattcaag	tc	aaagagg	tca	cgcagaatga	cggtagcag	acgattgcc	1860
cagcacg	gtt	cagggtgtt	ta	ctgactcgga	gtaccagctc	ccgtacgtcc	1920
gcatcaag	ga	tgctccccgc	cgtttccagc	ggacgtcttc	atgggtccac	agtatggata	1980
cctcac	cctg	aacaacggga	gtcaggcag	t	aggacgctct	tcattttact	2040
ctttcctt	ct	cagatgctgc	gtaccggaaa	caactttcaa	ttcagctaca	cttttgaaga	2100
cgtgcctt	ctt	cacagcagct	acgctcacag	ccagagtctg	gatcggctga	tgaatcctct	2160
ggctgac	cag	tac	ctgtatt	atctgaacaa	gacacaaaca	aatagtggaa	2220
gtctcgg	cta	ctgttttagcc	aagctggacc	caccaacatg	tctcttcaag	ctaaaaactg	2280
gctgcct	gga	ccttgctaca	gacagcagcg	tctgtcaaag	caggcaaacg	acaacaacaa	2340
cagcaact	ttt	ccctggactg	cagctacaaa	gtatcatcta	aatggccggg	actcgttgg	2400
taatccag	ga	ccagctatgg	ccagtcacaa	ggatgacgaa	gaaaagt	tttcccatgca	2460
tggaa	accctt	atatttggta	aacaagggaac	aaatgccaac	gacgcggatt	tggaaaatgt	2520
catgatt	taca	gatgaagaag	aaatcaggac	caccaatccc	gtggctacgg	agcagtacgg	2580
aactgtat	tca	aataatttgc	aaaactcaaa	cactggtcca	actactggaa	ctgtcaatca	2640
ccaaggag	c	gttac	ctggta	tgggtggga	ggatcgagac	gtgtacctgc	2700
ttgggcca	ag	attcctcaca	ccgatggaca	ctttcatcct	tctccactga	tgggaggttt	2760
tggactcaa	a	caccac	ctc	ctcaaatcat	gatcaaaaac	actcccgttc	2820
tcccacaa	ac	ttcagttctg	ccaagtttgc	ttctttcatc	acacagtatt	ccacggggca	2880
ggtcagc	gtg	gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	2940
aattcagt	tac	acttccaact	acaacaaatc	tg	ttaatgtg	gactttactg	3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt	3060
gcttgtaata caataaacccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc	3120
gaattcgttt aaacctgcag gactagtccc tttagtga	3158

<210> 171  
 <211> 3167  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.172.1

<400> 171	
attgaattta gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat	60
taaacggttt attgattaac aagcaattac agattacgag tcagggtacct ggtgccaatg	120
gggcgaggct ctgaatacac accattagtgt tccacagtaa agtccacatt aacagatttg	180
ttgtagtgtg aagtgtactg aatctcggga ttccagcggt tgctgttctc cttctgcagc	240
tcccactcga tctccacgct gacctgcccc gtggagtact gtgtaatgaa ggaagcaaac	300
tttgccgcac tgaaggtagt cgaaggattc gcagggtaccg ggggtgttctt gatgagaatc	360
tgcgggggag ggtgtttaaag tccgaatccg cccatgaggg gagaggggtg aaaatgtccg	420
tccgtgtgtg gaatctttgc ccagatgggc ccctgcagggt acacgtctct gtcctgccac	480
accatgcctg gaagaacgcc ttgtgtgttg acatctgagg tagctgcttg tgtgtgccc	540
ctctggagggt tggtagatac agaaccatac tgctccgtag ccacgggatt ggtggtcctg	600
atctctctct cgtctgtaat catgaccttt tcaatgtcca cattagtttt tcccagagtct	660
tgttttccaa agatgagaac cccgctctga ggaaaaaact tttcttcac gtccttggtg	720
ctggccatgg ccgggcccgg attcaccaga gagtctcttc cattaagggtg gtacttggtg	780
gctccagtcc acgagtattc actgtgtgtg ttatccgcag atgtctttga tactcgctgc	840
tggcggtaac aggggtccagg aagccagttc ctagactgggt cccgaatgtc acttgctccg	900
gcctgagaaa actgaagcct tgactgcgtg gtggttccgc ttggagtgtt tgttctgctc	960
aagtaataca ggtactgggtc gatgagagga ttcagtagac ggtccaaact ctggctgtgg	1020
gcgtagctgc tgtggaaagg aacgtcctca aagggtgtagc tgaaggtaaa gttgtttccg	1080
gtacgcagca tctgagaagg aaagtactcc aggcagtaaa atgaagagcg tcctactgcc	1140
tgactcccggt tgttcagggt gaggtatcca tactgtggca ccatgaagac gtctgctggg	1200
aacggcggga ggcacccctt atgcgccgag ccgaggacgt acgggagctg gtactccgag	1260
tcagtaaaca cctgaaccgt gctggttaagg ttattggcaa tcgctgctgt accgtcattc	1320
tgcgtgacct ctttgacttg aatgttaaag agcttgaagt tgagtctttt gggccggaat	1380
ccccaatgtt tgttgatgag tctttgccag tcacgtggcg aaaagtggca gtggaatctg	1440
ttgaagtcaa aataccccca aggggtgctg tagccaaagt agtgggtgtc gtttgaggct	1500
cctgattggc tggaaatctg cttgtagagg tgggtgttgt aggtgggcag agcccagggtg	1560
cgggtgctgg tgggtatgac tctgtcgccc atccatgtgg aatcgcaatg ccaatttccc	1620
gaggaattac cactccgctc ggcgcccctc ttattgtctg ccattggtgc gccactgcct	1680
gtagccatcg tattagtctc cagaccagag ggggtgctg gtggctgtcc gagaggctgg	1740
gggtcaggta cggagtctgc gtctccagtc tgaccgaaat tcaatctctt tcttgaggc	1800
tgctggcccc cttttccgggt tcccaggag gagtctggct ccgcaggaga gtgctctacc	1860
ggcctctttt tcccggagc cgtcttaaca ggttcctcaa ccaggcccag aggttcaaga	1920
accctctttt tcgcttgaa gactgctcgt ccgaggttgc ccccaaaaga cgtatcttct	1980
ttaagacgct cctggaactc cgcgtcggcg tgggtgtact tgggggtacgg gttgtctccg	2040

ctgtcgagct gccggctcgtg ggccttgctg tgctcgaggg ccgcggcgtc tgcctcgttg	2100
accggctctc ccttgctcgag tccgttgaag ggtccaaggt acttgtagcc aggaagcaca	2160
agacccttgc tgctgctcct atgccgtctt gcgggctttg gtggtggtgg gccaggtttg	2220
agcttccacc actgtcttat tccttcagag agagtgtcct cgagccaatc tggaagataa	2280
ccatcggcag ccatacctga tttaaactcat ttattgttca gagatgcagt catccaaatc	2340
cacattgacc agatcgcaag cagtgcgaag gtctggcacc tttcccatga tatgatgaat	2400
gtagcacagt ttctgatacg cctttttgac gacagaaacg ggttgagatt ctgacacggg	2460
aaagcactct aaacagtctt tctgtccgtg agtgaagcag atatttgaat tctgattcat	2520
tctctcgcat tgtctgcagg gaaacagcat cagattcatg cccacgtgac gagaacattt	2580
gttttggtac ctgtccgcgt agttgattga agcttccgcg tctgacgtcg atggctgcgc	2640
aactgactcg cgcgcccggt tgggctcact tatatctgcg tcaactgggg cggtctttt	2700
tttggtcca cctttttga cgtagaattc atgctctacc tcaaccacgt gatcctttgc	2760
ccaccgaaa aagtctttga cttcctgctt ggtgacctt ccaaagtcag gatccagacg	2820
gcgggtgagt tcaaatttga acatccggtc ttgcaacggc tgctggtgtt cgaaggtcgt	2880
tgagttcccc tcaatcactg cgcacatggt ggtgttgagg gtgacaatca cgggagtcgg	2940
gtctatctgg gccgaggact tgcatttctg gtccacgcgc accttgctt ctcgagaat	3000
ggctttggcc gactccacga ccttggcggc catcttcccc tcctcccacc agatcaccat	3060
cttgctgacg caatcattga aaggaaagtt ctcatgtgtc cagttgacgc agccgtagaa	3120
agggcgaatt cgtttaaacc tgcaggacta gtcccttag tgagggt	3167

<210> 172  
 <211> 3161  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.172.2

<400> 172	
aattgaattt agcggccgcg aattcgccct tcgcagagac caaagttcaa ctgaaacgaa	60
ttaaacgggt tattgattaa caagcaatta cagattacga gtcaggatc tggtgccaat	120
ggggcgaggc tctgaataca caccattagt gtccacagta aagtccacat taacagattt	180
gttgtagttg gaagtgtact gaatctcggg attccagcgt ttgctgttct ccttctgcag	240
ctccactcg atctccacgc tgacctgcc cgtaggagtag tgtgtaatga aggaagcaaa	300
ctttgccgca ctgaaggtag tcgaaggatt cgcaggtagc ggggtgttct tgatgagaat	360
ctgcggggga ggggtgttta gtccgaatcc gcccatgagg ggagaggggt gaaaatgtcc	420
gtccgtgtgt ggaatctttg ccagatggg cccctgcagg tacacgtctc tgtcctgcca	480
caccatgcct ggaagaacgc cttgtgtgtt gacatctgag gtagctgctt gtgtgttgcc	540
gctctggagg ttggtagata cagaaccata ctgctccgta gccacgggat tgggtgtcct	600
gatttcctct tcgtctgtaa tcatgacctt ttcaatgtcc acattagttt tccccagtc	660
ttgttttcca aagatgagaa ccccgtctg aggaaaaaac ttttcttcat cgtccttggt	720
gctggccatg gccgggccc gattcaccag agagtctctt ccattaagggt ggtacttggt	780
agctccagtc cacgagtatt cactgttgtt gttatccgca gatgtctttg atactcgtg	840
ctggcggtaa cagggtccag gaagccagtt cctagactgg tcccgaatgt cacttgctcc	900
ggcctgagaa aactgaagcc ttgactgcgt ggtggttccg cttggagtgt ttgttctgct	960
caagtaatac aggtactggt cgacgagagg attcatgaga cgggtccaaac tctggctgtg	1020

```

ggcgtagctg ctgtggaaag gaacgtcctc aaaggtgtag ctgaaggtaa agttgtttcc 1080
ggtacgcagc atctgagaag gaaagtactc caggcagtaa aatgaagagc gtcctactgc 1140
ctgactcccc ttgttcaggg tgaggatcc atactgtggc accatgaaga cgtctgctgg 1200
gaacggcggg aggcacacct gatgcgccga gccgaggacg tacgggagct ggtactccga 1260
gtcagtaaac acctgaaccg tgctggtgtaag gttattggca atcgtcgtcg taccgtcatt 1320
ctgcgtgacc tccttgactt gaatgttaaa gagcttgaag ttgagtcttt tgggccggga 1380
tcccccaattg ttgttgatga gtctttgcc gtcacgtggc gaaaagtggc agtggaatct 1440
gttgaagtca aaatacccc aaggggtgct gtagccaaag tagtggtgt cgtttgaggc 1500
tcctgattgg ctggaatct gcctgtagag gtggtgttg taggtggga gagcccagg 1560
gcggtgctg gtggtgatga ctctgtcgcc catccatgtg gaatcgcaat gccaatctc 1620
cgaggaatta cccactccgt cggcgccctc gttattgtct gccattggtg cgccactgcc 1680
tgtagccatc gtattagttc ccagaccaga gggggctgct ggtggctgtc cgagaggctg 1740
gggggtcagg acggagtctg cgtctccagt ctgaccgaaa ttcaatctcc ttcttgagg 1800
ctgctggccc gcttttcgg ttcccgagga ggagtctggc tccgcaagag agtgctctac 1860
cggcctcttt tttcccgag ccgtcttaac aggttcctca accaggccca gaggttcaag 1920
aaccctcttt ttcgcctgga agactgctcg tccgaggtt ccccaaaaag acgtatcttc 1980
tttaagacgc tcctggaact ccgctgcggc gtggtgttac ttgaggtagc ggttgtctcc 2040
gccgtcgagc tgccggtcgt aggccttgct gtgctcgagg gcccggcgt ctgcctcgtt 2100
gaccggctct ccctgtcga gtccgttgaa gggccaagg tacttgtagc caggaagcac 2160
aagaccctg ctgtcgtcct tatgccgtc tgcgggcttt ggtggtggtg ggccagggtt 2220
gagcttccac cactgtctta ttccttcaga gagagtgtc tcgagccaat ctggaagata 2280
accatcgga gccatactg atttaaatca ttattgttc agagatgcag tcatccaaat 2340
ccacattgac cagatcgcaa gcagtcaa gctctggcac ctttccatg atatgatgaa 2400
tgtagcacag tttctgatac gcctttttga cgacagaaac gggttgagat tctgacacgg 2460
gaaagcactc taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca 2520
ttctctcgca ttgtctgcag ggaaacagca tcagattcat gccacgtga cgagaacatt 2580
tgttttggt cctgtccgc tagttgattg aagcttccgc gtctgacgtc gatggctgcg 2640
caactgactc gcgcgcccgt ttgggtcac ttatatctgc gtcactggg gcgggtcttt 2700
ttttggctcc accctttttg acgtagaatt catgctctac ctcaaccacg tgatcctttg 2760
cccaccgaa aaagtctttg acttctgct tggtagcctt cccaaagtca tgatccagac 2820
ggcgggtgag ttcaaatgtg aacatccggt cttgcaacgg ctgctgggtg tcgaaggctg 2880
ttgagttccc gtcaatcact gcgcacatgt tgggtgttga ggtgacaatc acgggagtcg 2940
ggtctatctg ggccgaggac ttgcatttct ggtccacgcg caccttgctt cctccgagaa 3000
tggttttggc cgactccacg accttgccg tcatttccc ctctccac cagatcacca 3060
tctgtcgac gcaatcattg aaaggaaagt tctcattggt ccagttgacg cagcaagggc 3120
gaattcgttt aaacctgcag gactagtccc ttagtgagg g 3161

```

```

<210> 173
<211> 3172
<212> DNA
<213> Unknown

```

```

<220>
<223> new AAV serotype, clone hu.173.4

```

```

<400> 173
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

```

cccttcaacg	attgcgtcga	caagatggtg	atctggtggg	aggaggggcaa	gatgaccgcc	120
aaggctcgtg	agtcgcgcaa	ggccattctg	ggtggaagca	aggtgcgcgt	ggacaaaaag	180
tgcaagtcac	cggcccagat	cgacccacg	cccgtgatcg	tcacctccaa	caccaacatg	240
tgccgctga	tcgacgggaa	cagcaccacc	ttcgagcacc	agcagccctt	gcaggaccgc	300
atgttcaagt	tcgagctcac	ccgccgtctg	gagcacgact	ttggcaaggt	gaccaagcag	360
gaagtcгаа	agttcttccg	ctgggctcag	gatcacgtga	ctgagggtggc	gcatgagttc	420
tacgtcagaa	agggcggagc	cacaaaaaga	cccgcggcca	gtgacgcgga	tataagcgag	480
cccaagcggg	cctgccccct	agttgcggag	ccatcgacgt	cagacgcgga	agcaccggtg	540
gactttgcgg	acaggtacca	aaacaaatgt	tctcgtcacg	cgggcatgct	tcagatgctg	600
tttcctgca	agacatgcga	gagaatgaat	cagaatttca	acgtctgctt	cacgcacggg	660
gtcagagact	gctcagagtg	cttccccggc	gcgtcggaat	ctcaaccctg	cgtcagaaaa	720
aagacgtatc	agaaactgtg	cgcgattcat	catctgctgg	ggcgggcacc	cgagattgcy	780
tgttcggcct	gcgatctcgt	caacgtggac	ttggatgact	gtgtttctga	gcaataaatg	840
acttaaacca	ggtatggctg	ctgacgggta	tcttccagat	tggtcgcagg	acaacctctc	900
tgagggcatt	cgcgagtggg	gggacctgaa	acctggagcc	cccaagccca	aggccaacca	960
gcagaagcag	gacgacggcc	ggggctctgt	gcttctggc	tacaagtacc	tcggaccctt	1020
caacggactc	gacaaggggg	agcccgtcaa	cgcggcggac	gcagcggccc	tcgagcacga	1080
caaggcctac	gaccagcagc	tcaaagcggg	tgacaatccg	tacctgcggt	ataaccacgc	1140
cgacgccgag	tttcaggagc	gtctgcaaga	agatacgtct	tttgggggca	acctcgggcy	1200
agcagtcttc	caggccaaga	agcgggttct	cgaacctctc	ggtctggttg	aggaagctgc	1260
taagacggct	cctggaaaga	agagaccggt	agaaccgtca	cctcagcggt	cccccgactc	1320
ctccgcgggc	atcggaaga	aaggccagca	gcccgcataa	aagagactga	actttggtca	1380
gactggcgac	tcagagtcag	tccccgacct	tcaaccaatc	ggagaaccac	cagcaggccc	1440
ctctggctcg	ggatctggta	caatggctgc	aggcgggtgg	gctccaatgg	cagacaataa	1500
cgaaggcgcc	gacggagtgg	gtagtctctc	aggaaattgg	cattgcgatt	ccacatggct	1560
gggcgacaga	gtcatcacca	ccagcaccgc	aacctggggc	ctgcccacct	acaacaacca	1620
cctctacaag	caaatatcca	atgggacatc	gggaggaagc	accaacgaca	acacctactt	1680
cggctacagc	acccccctgg	ggtattttga	cttcaacaga	ttccactgcc	acttctcacc	1740
acgtgactgg	cagcgactca	tcaacaacaa	ctggggattc	cggccaaaaa	gactcagctt	1800
caagctcttc	aacatccagg	tcaaggaggt	cacgcagaat	gaaggcaccg	agaccatcgc	1860
caataacctt	accagcacga	ttcagggtatt	tacggactcg	gaataccagc	tgccgtacgt	1920
cctcggctcc	gcgcaccagg	gctgcctgcc	tccgttcccc	gcggacgtct	tcattgattcc	1980
ccagtacggc	taccttacac	tgaacaatgg	aagtcaagcc	gtaggccggt	cctccttcta	2040
ctgcctggaa	tattttccat	ctcaaatgct	gcgaactgga	aacaattttg	aattcagcta	2100
caccttcgag	gacgtgcctt	tccacagcag	ctgcgcacac	agccagagct	cggaccgact	2160
gatgaatcct	ctcatcgacc	agtacctgta	ctacttatcc	agaactcggg	ccacaggagg	2220
aactcaaggt	acccagcaat	tggtattttc	tcaagctggg	cctgcaaaca	tgctggctca	2280
ggctaagaac	tggtacctg	gaccttgcta	ccggcagcag	cgagtctcta	cgacactgtc	2340
gcaaaacaac	aacagcaact	ttgcttgga	tggtgccacc	aaatatcacc	tgaacggaag	2400
agactctttg	gtaaatcccc	gtgtcgccat	ggcaaccac	aaggacgacg	aggaacgctt	2460
cttcccgctg	agtggaagtcc	tgatgtttgg	aaaacagggt	gctggaagag	acaatgtgga	2520

ctacagcagc gttatgctaa ccagcgaaga agaaattaaa accactaacc ctgtagccac	2580
agaacaatac ggtgtggtgg ctgacaactt gcagcaaac aatacagggc ctattgtggg	2640
aatgtcaac agccaaggag ccttacctgg catggtctgg cagaaccgag acgtgtacct	2700
gcaggggtccc atctggggcca agattcctca cacggacggc aacttccacc cttcacgct	2760
aatgggagga tttggactga agcaccacc tcctcagatc ctgatcaaga acacgccggt	2820
acctgcggat cctccaacaa cgttcagcca ggcgaaattg gcttccttca ttacgcagta	2880
cagcaccgga caggtcagcg tggaaatcga gtgggagctg cagaaggaga acagcaaacg	2940
ctggaaccca gagattcagt acacttcaaa ctactacaaa tctacaaatg tggactttgc	3000
tgtcaatata gagggaaactt attctgagcc tcgccccatt ggtactcggt acctcacccg	3060
taatctgtaa ttgctggtta atcaataaac cgtttgattc gtttcagttg aactttggtc	3120
tctgcgaagg gcgaattcgt ttaaacctgc aggactagtc cctttagtga gg	3172

<210> 174  
 <211> 3159  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.161.8

<400> 174	
gattgaattt agcggccgcg aattcgccct tgctgctga actggaccaa tgagaacttt	60
cctttcaatg attgctcga caagatggtg atctggtggg aggagggaaa gatgaccgcc	120
aaggctcgtg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa	180
tgcaagtcct cggcccagat agaccgact cccgtgattg tcacctcaa caccgacatg	240
tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg	300
atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag	360
gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc	420
tacgtcaaaa aggggtggagc taagaaaaga cccgccccca gtgacgcaga tataagtgag	480
cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc	540
aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg	600
tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga	660
cagaaagact gtttagagtg ctttcccgtg tcagaatctc aaccggtttc tgtcgtcaaa	720
aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc	780
actgcctcgc atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt	840
taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga	900
aggaataaga cagtgtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg	960
gcataaggac gacagcaggg gtcttggtgt tcctgggtac aagtacctcg gaccttcaa	1020
cggactcgac aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa	1080
ggcctacgac cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga	1140
cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc	1200
agtcttccag gcaaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa	1260
aacggctccg ggaaaaaaga ggccggtaga gcacctcct gtggagccag actcctcctc	1320
gggaaccgga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg	1380
agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg	1440
tctgggatct actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg	1500
tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga	1560

cagagtcatc accaccagca cccgcacctg ggccttgccc acctacaaca accacctcta	1620
caagcaaadc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac	1680
cccctggggg tattttgact tcaacagatt ccaactgccac ttttcaccac gtgactggca	1740
aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa	1800
cattcaagtc aaagagggtca cgcagaatga cggtagcagc acgattgccg ataaccttac	1860
cagcacgggt cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc	1920
gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atggtccac agtatggata	1980
cctcacctg aacaacggga gtcaggcagt aggacgtctc tcattttact gcctggagta	2040
ctttccttct cagatgctgc gtaccggaaa caactttcag ttcagctaca cttttgaaga	2100
cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct	2160
gatcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca	2220
gtctcggcta ctgttttagc aagctggacc caccaacatg tctcttcaag ctaaaaaccg	2280
gctgcctgga ccttgctaca gacagcagc tctgtcaaag caggcaaacg acaacaacaa	2340
cagcaacttt ccctggaccg cagctacaaa gtatcatcta aatggccggg actcgttggt	2400
taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagttt tccccatgca	2460
tgggaaccctt atatttggtg aacaaggaac aaatgccaac gacgcggatt tggaaaatgt	2520
catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg	2580
aactgtatca aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca	2640
ccaaggagcg ttacctggta tgggttgcca ggatcgagac gtgtacctgc agggacccat	2700
ttgggccaaag attcctcaca ccgatggaca ctttcacctc tctccactgg tgggaggttt	2760
tggactcaaa caccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc	2820
tcccacaaac tttagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca	2880
ggtagcagtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga	2940
aattcagtag acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa	3000
tgggtgtgat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt	3060
gcttggtaat caataaaccg ttttaattcgt ttcagttgaa ctttggtctc tgccaagggc	3120
gaattcgttt aaacctgcag gactagctcc tttagttag	3159

<210> 175  
 <211> 3172  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.173.8

<400> 175	
gattgaattt agcgccgcg aattcgccct tgctgctga actggaccaa tgagaacttt	60
cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgaccgcc	120
aaggctcgtg agtccgccaa ggccattctg ggtggaagca aggtgcgcgt ggaccaaag	180
tgcaagtcac cggcccagat cgacccacg cccgtgatcg tcacctcaa caccaacatg	240
tgccgctga tcggcgggaa cagcaccacc ttcgagcacc agcagccct gcaggaccgc	300
atgttcaagt tcgagctcac ccgccgtctg gagcacgact ttggcaagg gaccaagcag	360
gaagtc aaag agttcttccg ctgggctcag gatcacgtga ctgaggtggc gcatgagttc	420
tacgtcagaa agggcggagc caccaaaaga cccgccccca gtgacgcgga tataagcgag	480
cccaagcggg cctgcccctc agttgcggag ccatcgacgt cagacgcgga agcaccgggtg	540

gactttg	cgg	acaggtacca	aaacaaatgt	tctcgtcacg	cgggcatgct	tcagatgctg	600
tttccctgca	agacatgcga	gagaatgaat	cagaatttca	acgtctgctt	cacgcacggg		660
gtcagagact	gctcagagt	cctccccggc	gcgtcagaat	ctcaacccgt	cgtcagaaaa		720
aagacgtatc	agaaactgtg	cgcgattcat	catctgctgg	ggcgggcacc	cgagattgcg		780
tgttcggcct	gcgatctcgt	caacgtggac	ttggatgact	gtgttttctga	gcaataaatg		840
acttaaacca	ggatatggctg	ctgacggtta	tcttccagat	tggctcgagg	acaacctctc		900
tgagggcatt	cgcgagtgg	gggacctgaa	acctggagcc	ccaagccca	aggccaacca		960
gcagaagcag	gacgacggcc	ggggtctggt	gcttcttggc	tacaagtacc	tcggaccctt		1020
caacgggactc	gacaaggggg	agccccgtcaa	tgcggcggac	gcagcggccc	tcgagcacga		1080
caaggcctac	gaccagcagc	tcaaagcggg	tgacaatccg	tacctgcggt	ataaccacgc		1140
cgacgcccag	tttcaggagc	gtctgcaaga	agatacgtct	tttgggggca	acctcgggcg		1200
agcagtcttc	caggccaaga	agcgggttct	cgaacctctc	ggtctggttg	aggaagctgc		1260
taagacggct	cctggaaaga	agagaccggt	agaacctgca	cctcagcggt	cccccgactc		1320
ctccacgggc	atcggaaga	aaggccagca	gcccgtaaa	aagagactga	actttggtca		1380
gactggcgac	tcagagtcag	tccccgacct	tcaaccaatc	ggagaaccac	cagcaggccc		1440
ctctgggtctg	ggatctggta	caatggctgc	aggcgggtggc	gctccaatgg	cagacaataa		1500
cgaagcgccc	gacggagtgg	gtagttcctc	aggaaattgg	cattgcgatt	ccacatggct		1560
gggcgacaga	gtcatcacca	ccagcaccgc	aacctggggc	ctgcccacct	acaacaacca		1620
cctctacaag	caaatatcca	atgggacatc	gggagggaagc	accaacgaca	acacctactt		1680
cggctacagc	accccctggg	ggatatttga	cttcaacaga	ttccactgcc	acttctcacc		1740
acgtgactgg	cagcgactca	tcaacaacaa	ctggggattc	cggccaaaaa	gactcagctt		1800
caagctcttc	aacatccagg	tcaaggaggt	cacgcagaat	gaaggcacca	agaccatcgc		1860
caataacctt	accagcacga	ttcagggtatt	tacggactcg	gaataaccagc	tgccgtacgt		1920
cctcggctcc	gcgcaccagg	gctgcctgcc	tccgttccc	gcggacgtct	tcattgattcc		1980
ccagtacggc	taccttacac	tgaacaatgg	aagtcaagcc	gtaggccggt	cctccttcta		2040
ctgcctggaa	tattttccat	ctcaaagtct	gcgaactgga	aacaattttg	aattcagcta		2100
caccttcgag	gacgtgcctt	tccacagcgg	ctacgcacac	agccagagct	tggaccgact		2160
gatgaatcct	ctcatcgacc	agtacctgta	ctacttatcc	agaactcagt	ccacaggagg		2220
aactcaaggt	acccagcaat	tggtattttc	tcaagctggg	cctgcaaaca	tgctcggctca		2280
ggctaagaac	tggctacctg	gaccttgcta	ccggcagcag	cgagtctcta	cgacactgtc		2340
gcaaaacaac	aacagcaact	ttgcttggac	tggtgccacc	aaatatcacc	tgaacggaag		2400
agactctttg	gtaaatccc	gtgtcgccat	ggcaacccac	aaggacgacg	aggaacgctt		2460
cttcccgtcg	agtggagtcc	tgatgtttgg	aaaacagggt	gctggaagag	acaatgtgga		2520
ctacagcagc	gttatgctaa	ccagcgaaga	agaaattaaa	accactaacc	ctgtagccac		2580
agaacaatac	gggtgtggtg	ctgacaactt	gcagcaaac	aatacagggc	ctattgtggg		2640
aaatgtcaac	agccaaggag	ccttacctgg	catggtcttg	cagaaccgag	acgtgtacct		2700
gcagggtccc	atctgggcca	agattcctca	cacggacggc	aacttccacc	cttcaccgct		2760
aatgggagga	tttggactga	agcaccaccc	tcctcagatc	ctgatcaaga	acacgcgggt		2820
acctcgggat	cctccaacga	cgttcagcca	ggcgaattg	gcttccttca	ttacgcagta		2880
cagcaccgga	caggtcagcg	tggaaatcga	gtgggagctg	cagaaggaga	acagcaaacg		2940
ctggaaccca	gagattcagt	acacttcaaa	ctactacaaa	tctacaaatg	tggactttgc		3000
tgtcaataca	gagggaaactt	attctgagcc	tcgccccatt	ggtactcggt	acctcaccgc		3060

taatctgtaa ttgctgggta atcaataaac cgtttgattc gtttcagttg aactttggtc	3120
tctgCGaagg gcgaattcgt ttaaacctgc aggactagtc cctttagtga gg	3172

<210> 176  
 <211> 3160  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.145.1

<400> 176	
acccttcact aaagggacta gtcctgcagg tttaaacgaa ttcgcccttg ctgcgtcaac	60
tggaccaatg agaactttcc cttcaacgac tgtgtcgaca agatggtgat ttggtgggag	120
gaggggaaga tgaccgccaa ggtcgtggag tcggccaaag ccatttctcg aggaagcaag	180
gtgcgcgtgg accagaaatg caagtcctcg gccagatag atccgactcc cgtgatcgtc	240
acctccaaca ccaacatgtg cgccgtgatt gacgggaact caacgacctt cgaacaccag	300
cagccgttgc aagaccggat gttcaaattt gaactcacc gccgtctgga tcatgacttt	360
gggaagggtca ccaagcggga agtcaaaagac tttttccggg gggcaaagga tcacgtgggt	420
gaggtggagc atgaattcta cgtcaaaaag ggtggagcca agaaaagacc cgcccctagt	480
gacgcagata taagtgaagg caaacgggtg cgcgagtcag ttgcgcagcc atcgacgtca	540
gacgcggaag cttc gatcaa ctacgcggac aggtaccaa acaaatgttc tcgtcacgtg	600
ggcatgaatc tgatgctgtt tccctgcaga caatgcgaga gaatgaatca aaattcaaat	660
atctgcttca ctcacggaca gaaagactgt ttagagtgtt tccccgtgtc agaattctca	720
cctgtttctg tcgtcaaaaa ggcgtatcag aaactgtgtt acattcatca tatcatggga	780
aaggtgccag acgcttgac tgcctgcgat ctggtcaatg tggatttggg tgactgcatc	840
tctgaacaat aaatgattta aatcagggtat ggctgccgat gggtatcttc cagattgggt	900
cgaggacact ctctctgaag gaataagaca gtggtggaag ctcaaacctg gccaccacc	960
accaaagccc gcagagcggc ataaggacga cagcaggggt cttgtgcttc ctgggtacaa	1020
gtacctcgga ccttcaacg gactcgacaa gggagagccg gtcaacgagg cagacgccgc	1080
ggccctcgag cagcacaagg cctacgaccg gcagctcgac agcggagaca acccgtaçct	1140
caagtacaac cagcggcagc cgaggtttca ggagcgtctt aaagaagata cgtcttttgg	1200
gggcaacctc ggacgagcag tcttccaggc gaaaaagagg gttcttgaac ctctgggcct	1260
ggttgaggaa cctgttaaga cggctccggg aaaaagagg ccggtagagc actctcctgc	1320
ggagccagac tcctcctcgg gaaccggaaa agcggggccag cagcctgcaa gaaaaagact	1380
gaatttcggt cagactggag acgcagactc cgtacctgac cccagcctc tcagacagcc	1440
accagcagcc cccacaagtt tgggatctac tacaatgggt acaggcagtg gcgcaccaat	1500
ggcagacaat aacgaggggt ccgatggagt gggtaattcc tcaggaaatt ggcattgcga	1560
ttcccaatgg ctgggcgaca gagtcacac caccagcacc cgaacctggg ccctgcccac	1620
ctacaacaac cacctttaca agcaaatctc cagccaatca ggagcctcaa acgacaacca	1680
ctactttggc tacagcacc cctgggggta ttttgacttc aacagattcc actgccactt	1740
ttcaccacgt gactggcaaa gactcatcaa caacaactgg ggattccgac ccaagagact	1800
caacttcaag ctctttaaca ttcaagtcaa agaggtcacg cagaatgacg gtacgacgac	1860
gattgccaat aaccttacca gcacggttca ggtgtttact gactcggagt accagctccc	1920
gtacgtcctc ggctcggcgc atcaaggatg cctcccgccg tttccagcgg acgtcttcat	1980
ggccccacag tatggatacc tcaccctgaa caacgggagt caggcggtag gacgtcttcc	2040



tcgagcacga caaggcctac gaccggcagc tcgacagcgg agacaacccg tacctcaagt	1140
acaaccacgc cgacgcggag ttctcaggagc gtcttaaaga agatacgtct tttgggggca	1200
acctcggacg agcagtcctc caggcgaaaa agaggggttct tgaacctctg ggcctggttg	1260
aggaacctgt taagacggct ccgggaaaaa agaggccggg agagcactct cctgcggagc	1320
cagactcctc ctcgggaacc ggaaaagcgg gccagcagcc tgcaagaaaa agactgaatt	1380
tcggtcagac tggagacgca gactccgtac ctgacccccca gcctctcggg cagccaccag	1440
cagcccccac aagtttgga tctactacaa tggctacagg cagtggcgca ccaatggcag	1500
acaataacga ggggtgccgat ggagtgggta attcctcagg aaattggcat tgcgattccc	1560
aatggctggg cgacagagtc atcaccacca gaccccgaa ctggggccctg cccacctaca	1620
acaaccacct ttacaagcaa atctccagcc aatcaggagc ctcaaacgac aaccactact	1680
ttggctacag caccctctgg ggggtattttg acttcaacag attccactgc cgcttttcac	1740
cacgtgactg gcaaagactc atcaacaaca actgggggatt ccgacccaag agactcaact	1800
tcaagctctt taacattcaa gtcaaagagg tcacgcagaa tgacggtacg acgacgattg	1860
ccaataacct taccagcacg gttcagggtg ttactgactc ggagtaccag ctcccgtacg	1920
tcctcggctc ggcgcataca ggatgcctcc cgccgtttcc agcggacgtc ttcattgtcc	1980
cacagtatgg atacctcacc ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt	2040
actgcctgga gtactttcct tctcagatgc tgcgtactgg aaacaacttt cagttcagct	2100
acacttttga agacgtgcct ttccacagca gctacgtcga cagccagggt ttggatcggc	2160
tgatgaatcc tctgatcgac cagtacctgt attatctaaa cagaacacaa acagctagt	2220
gaactcagca gtctcggcta ctgtttagcc aagctggacc cacaagcatg tctcttcaag	2280
ctaaaaactg gctgcctgga ccgtgttatc gccagcagc tttgtcaaag caggcaaacg	2340
acaacaacaa cagcaacttt ccctggactg gagctaccaa gtaccacctc aatggcggag	2400
actcttttgt gaaccgggc ccggccatgg ccagccacaa ggacgatgaa gaaaagt	2460
tccccatgca tggaaacctc atatttggtg aagaaggaa aaatgctacc aacgcggaat	2520
tggaaaatgt catgattaca gatgaagagg aaatcaggac caccaatccc tgggctacag	2580
agcagtacgg atatgtgtca aataatttgc aaaactcaaa tactgctgca agtactgaaa	2640
ctgtgaatca ccaaggagca ttacctggta tgggtgtggca ggatcgagac gtgtacctgc	2700
ggggacccat ttgggccaag attcctcacg ccgatggaca ctttcacctc tctccactga	2760
tggggaggtt tggactcaaa caccgcctc ctcagattat gatcaaaaac actcccgttc	2820
cagccaatcc tcccacaaac ttcagttctg ccaagtttgc ttccttcac acacagtatt	2880
ccacgggaca ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct	2940
ggaatcccga aattcagtag acttccaact acaacaaatc tgtaaatgtg gactttactg	3000
tggacactaa tgggtgtgtat tcagagcctc gcccattgg caccagatac ctgactcgta	3060
atctgtaatt gcttgtaaat caataaacg ttttaattcgt ttcagttgaa ctttggtctc	3120
tgcgaagggc gaattcgcg ccgctaaatt caattcg	3157

<210> 178  
 <211> 3163  
 \*212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.145.6

<400> 178	
acctcacta aagggactag tcctgcagg ttaaacgaat tcgcccttgc tgcgtcaact	60

ggagcaatga gaactttccc ttcaacgact gtgtcgacaa gatggtgatt tgggtgggagg	120
aggggaagat gaccgccaag gtcgtggagt cggccaaagc cattctcgga ggaagcaagg	180
tgcgcgtgga ccagaaatgc aagtcctcgg cccagataga tccgactccc gtgatcgtca	240
cctccaacac caacatgtgc gccgtgattg acgggaactc aacgaccttc gaacaccagc	300
agccgttgca agaccggatg ttcaaatttg aactcacccg ccgtctggat catgactttg	360
ggaagggtcac caagcaggaa gtcaaagact ttttccggtg ggcaaaggat cacgtgggtg	420
aggtggagca tggattctac gtcaaaaagg gtggagccaa gaaaagaccc gcccttagtg	480
acgcagatat aagttagccc aaacgggtgc gcgagtcagt tgcgcagcca tcgacgtcgg	540
acgcggaagc ttcgatcaac tacgcggaca ggtacaaaaa caaatgttct cgtcacgtgg	600
gcataaatct gatgctgttt ccctgcagac aatgcgagag aatgaatcaa aattcaaata	660
tctgtttcac tcacggacag aaagactggt tagagtgttt tcccgtgtca gaatctcaac	720
ctgtttctgt cgtcaaaaag gcgtatcaga aactgcgcta cattcatcat atcatgggaa	780
aggtgccaga cgcttgcaact gcctgcgacg tggtaaatgt ggatttggat gactgcatct	840
ctgaacaata aatgatttaa atcaggtatg gctgccgatg gttatcttcc agattggctc	900
gaggacactc tctctgaagg aataagacag tgggtggaag tcaaacctgg cccaccacca	960
ccaaagcccg cagagcggca taaggacgac agcaggggtc ttgtgcttcc tgggtacaag	1020
tacctcgga ccttcaacgg actcgacaag ggagagccgg tcaacgaggc agacgccggc	1080
gccctcgagc acgacaaggc ctacgaccgg cagctcgaca gcggagacaa cccgtacctc	1140
aagtacaacc acgccgacgc ggagtctcag gagcgtctta aagaagatac gtcttttggg	1200
ggcaacctcg gacgagcagt cttccaggcg aaaaagaggg ttcttgaacc tctgggcctg	1260
gttgaggaa cgtttaagac ggctccggga aaaaagaggc cggtagagca ctctcctgcg	1320
gagccagact cctcctcggg aaccggaaaa gcgggcccagc agcctgcaag aaaaagactg	1380
aatttcggtc agactggaga cgcagactcc gtacctgacc cccagcctct cggacagcca	1440
ccagcagccc ccacaagttt gggatctact acaatggcta caggcagtg cgcaccaatg	1500
gcagacaata acgagggtgc cgatggagtg ggtaattcct caggaaattg gcattgcgat	1560
tcccaatggc tgggcgacag agtcacacc accagacccc gaacctgggc cctgcccacc	1620
tacaacaacc acctttacaa gcaaattctc agccaatcag gagcctcaaa cgacaaccac	1680
tactttggct acagcaccac ctgggggtat ttgacttca acagattcca ctgccacttt	1740
tcaccacgtg actggcaaag actcatcaac aacaactggg gattccgacc caagagactc	1800
aacttcaagc tctttaacat tcaagtcaaa gaggtcacgc agaatgacgg tacgacgacg	1860
attgccaata accttaccag cacggttcag gtgtttactg actcggagta ccagctcccg	1920
tacgtcctcg gctcggcgca tcaaggatgc ctcccgccgt ttccagcggg cgtcttcatg	1980
gtcccacagt atggatacct caccctgaac aacgggagtc aggcggtagg acgctcttcc	2040
ttttactgcc tggagtgttt tccttctcag atgtgctgta ctggaacaa ctttcagttc	2100
agctacactt ttgaagacgt gcctttccac agcagctacg ctcacagcca gagtttggat	2160
cggctgatga atcctctgat cgaccagtac ctgtattatc taaacagaac acaaacagct	2220
agtggaaact agcagtcctg gctactgttt agccaagctg gaccacaag catgtctctt	2280
caagctaaaa actggctgcc tggaccgtgt tatcgccagc agcgtttgtc aaagcaggca	2340
aacgacaaca acaacagcaa ctttccctgg actggagcta ccaagtacca cctcaatggc	2400
agagactcct tgggtgaaccc gggcccggcc atggccagcc acaaggacga tgaagaaaag	2460
tttttcccca tgcattggaac cctaataattt ggtaaagaag gaacaaatgc taccaacgcg	2520
gaattggaaa atgtcatgat tacagatgaa gaggaatatc ggaccaccaa tcccgtggct	2580

acagagcagt acggatatgt gtcaaataat ttgcaaaact caaatactgc tgcaagtact	2640
gaaactgtga atcaccaagg agcattacct ggtatggtgt ggcaggatcg agacgtgtac	2700
ctgcagggac ccatttgggc caagattcct cacaccgatg gacactttca tccttctcca	2760
ctgatgggag gttttggact caaacacccg cctcctcaga ttatgatcaa aaacactccc	2820
gttccagcca atcctccac aaacttcagt tctgccaagt ttgttcctt catcacacag	2880
tattccacgg gacaggtcag cgtggagatc gagtgggagc tgcagaagga gaacagcaaa	2940
cgctggaatc ccgaaattca gtacacttcc aactacaaca aatctgttaa tgtggacttt	3000
actgtggaca ctaatggtgt gtattcagag cctcgcccca ttggcaccag atacctgact	3060
cgtaatctgt aattgcttgt taatcaataa accgtttaat tcgtttcagt tgaactttgg	3120
tctctgcgaa gggcgaattc gcggccgcta aattcaattc gcc	3163

<210> 179  
 <211> 3161  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.156.1

<400> 179	
cgaattgatt tagcgccgc gaattcgccc ttcgcagaga ccaaagtcca actgaaacga	60
attaaacggt ttattgatta acaagcaatt acagattacg agtcaggat ctggtgcca	120
tggggcgagg ctctgaatac acaccattag tgtccacagt aaagtccaca ttaacagatt	180
tgtttagatt ggaagtgtac tggatctcgg gattccagcg tttgctgttc tccttctgta	240
gctcccactc gatctccacg ctgacccgcc ccgtggaata ctgtgtgatg aaggaagcaa	300
actttgccgc actgaagggt gtcgaaggat tcgcaggatc cgggggtgtt ttgatgagaa	360
tctgtggagg aggggtgtta agtccgaatc cgcccatgag gggagagggg tgaaaatgtc	420
cgtccgtgtg cggaatcttt gccagatag gccctgcag gtacacgtct ctgtcctgcc	480
agaccatgcc tggaagaacg ccttgtgtgt tgacatctgc agtagatgct tgtgtgttgc	540
cgtcttggag gttggtagat acagaacat actgtctcgt ggccacggga ttggtggttc	600
tgatttcttc ttcgtctgta atcatgacct tttcaatgtc cacatttgtt ttctctgac	660
cttgttttcc aaagatgaga accccgctct gaggaaaaaa cttttcttca tcgtccttgt	720
ggctggccat tgccgggccc ggattcacca gagagtctct gccattgagg tggacttgg	780
tagctccaat ccacgagtat tcaactgtgt tgttgtccgc agatgtcttt gatactcgt	840
gctggcggta acaggggtcca ggaagccagt tcctagactg atcccgaatg tcaactcgtc	900
cggcctgaga aaactgaagc ctggactgcg tgggtgttcc gcttggagtg tttgttctgc	960
tcaagtaata cagggtactg tcgatgagag gattcatgag acggtccaaa ctctggctgt	1020
gagcgtagct gctgtggaag ggaacatcct caaagggtga gctgaaggta aagttgtttc	1080
cggtagcgag catctgagaa gggaggtact ccaggcagta aaatgaagag cgtcctactg	1140
cctgactccc gttgttcagg gtgaggtatc catactgtgg caccatgaag acgtctgctg	1200
ggaacggcgg gaggcatcct tgatgcgccg agccgaggac gtacgggagc tgggtactccg	1260
agtcagtaaa cacctgaacc gtgctggtaa ggttattggc aatcgtcgtc gtaccatcat	1320
tctgcgtgac ctctctgact tgaatgttaa agagcttgaa gttgagtctc ttgggccgga	1380
atccccagtt gttgttgatg agtctttgcc agtcacgtgg tgaaaagtgg cagtggaatc	1440
tgttgaagtc aaaatacccc caaggggtgc tgtagccaaa gtagtggttg tcgttgctgg	1500
ctcctgattg gctggaaatc tgctgtgaca gatggttgtt gtaggtgggc agagcccagg	1560

ttcgggtgct ggtggtgatg actctgtcgc ccatccatgt ggaatcgcaa tgccaatttc	1620
ccgaggaatt acccactccg tcggcgccat cgttattgtc tgccattggt gcgccactgc	1680
ctgtagccat cgtattagtt cccagaccag agggggctgc tgggtggctgt ccgagaggct	1740
gggggtcagg tacggagtct gcgtctccag tctgaccgaa attcaatctc tttcttgca	1800
gctggttgcc cgcttttccg gttccccgag aggagtctgg ctccacagga gagtgtctta	1860
ccggcctctt ttttcccgga gccgtcttaa caggctcctc aaccaggccc agagggtcaa	1920
gaaccctctt ttttgctgga aagactgctc gtccgagggt gccccaaaa gacgtatctt	1980
ctttaaggcg ctcttgaaac tccgcgtcgg cgtggtcgta cttgaggtag gggttgtctc	2040
cgctgtcag ctgccggtcg taggccttgt cgtgctcgag ggccgcggcg tctgcctcgt	2100
tgaccggctc tcccttgctg agtccgttga aggggtccgag gtactgttac ccaggaagca	2160
caagaccctt gctgtcgtcc ttatgccgct ctgcgggctt tgggtgggtgt gggccagggt	2220
tgagcttcca cactgtctt attccttcag agagagtgtc ctcgagccaa tctggaagat	2280
aaccatcggc agccatacct gatttaaattc atttattgtt cagagatgca gtcattccaa	2340
tccacattga ccagatcgca ggcagtgcga gcgtctggca cctttcccat gatattgatga	2400
atgtagcaaa gtttctgata cgcctttttg acgacagaaa cgggttgaga ttctgacacg	2460
ggaaagcact ctaaacagtc tttctgtccg tgagtgaagc agatatttga attctgattc	2520
attctctcgc attgtctgca gggaaacagc atcagattca tgcccacgtg acgagaacat	2580
ttgttttggg acctgtccgc gtagttgatc gaagcttccg cgtctgacgt cgatggctgc	2640
gcaactgact cgcgcgcccc tttgggtcga cttatatctg cgtcactggg ggcgggtctt	2700
ttcttggtc cacccttttt gacgtagaat tcatgtcca cctcaaccac gtgatccttt	2760
gccccaccga aaaagtcttt cacttcctgc ttggtgacct tcccaaagtc atgatccaga	2820
cggcgggtta gttcaaatth gaacatccgg tcttgcaacg gctgctgggtg ttcgaaggtc	2880
gttgagttcc cgtcaatcac ggcgcacatg ttggtgttgg aggtggcgat cacgggagtc	2940
gggtctatct gggccgagga cttgcacttt tgggtccacgc gcacctgtct tcctccgaga	3000
atggcttcgg ccgattccac gacctggcg gtcattcttc cctcctccca ccagatcacc	3060
atcttgctga cacagtcgtt gaagggaag ttctcattgg tccagttgac gcagcaaggg	3120
cgaattcgtt taaacctgca ggaactagtc ccttagtgag g	3161

<210> 180  
 <211> 4721  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 7

<400> 180	
ttggccactc cctctatgct gcgtcgctcg ctccggtggg cctgcggacc aaagggtccgc	60
agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcat agagggagtg	120
gccaactcca tctagggg taccgcgaag cgcctccac gctgccgct cagcgctgac	180
gtaaatcacg tcatagggga gtggtcctgt attagctgtc acgtgagtgc ttttgcgaca	240
ttttgcgaca ccacgtggcc atttgaggta tatatggccg agtgagcgag caggatctcc	300
attttgaccg cgaaatttga acgagcagca gccatgccgg gtttctacga gatcgtgac	360
aagggtgccg gcgacctgga cgagcacctg ccgggcattt ctgactcgtt tgtgaactgg	420
gtggccgaga aggaatggga gctgcccccg gattctgaca tggatctgaa tctgatcgag	480
caggcacccc tgaccgtggc cgagaagctg cagcgcgact tcctgggtcca atggcgccgc	540
gtgagtaagg ccccgaggc cctgttcttt gttcagttcg agaagggcga gagctacttc	600

caccttcacg	ttctggtgga	gaccacgggg	gtcaagtcca	tgggtgctagg	ccgcttcctg	660
agtcagattc	gggagaagct	ggtccagacc	atctaccgcg	gggtcgagcc	cacgctgccc	720
aactggttcg	cggtgaccaa	gacgcgtaat	ggcgccggcg	gggggaacaa	ggtggtggac	780
gagtgtctaca	tccccaacta	cctcctgccc	aagaccagc	ccgagctgca	gtgggctgg	840
actaacatgg	aggagtatat	aagcgcgtgt	ttgaacctgg	ccgaacgcaa	acggctcgtg	900
gcgcagcacc	tgaccacagt	cagccagacg	caggagcaga	acaaggagaa	tctgaacccc	960
aattctgacg	cgcccgtgat	caggtcaaaa	acctccgcgc	gctacatgga	gctggctggg	1020
tggctggtgg	accggggcat	cacctccgag	aagcagtgga	tccaggagga	ccaggcctcg	1080
tacatctcct	tcaacgccgc	ctccaactcg	cggtcccaga	tcaaggccgc	gctggacaat	1140
gccggcaaga	tcatggcgct	gaccaaatcc	gcgcccgaact	acctggtggg	gccctcgtcg	1200
cccgcggaca	ttaaaaccaa	ccgcattctac	cgcatcctgg	agctgaacgg	gtacgatcct	1260
gcctacgccg	gctccgtctt	tctcggctgg	gccagaaaa	agttcgggaa	gcgcaacacc	1320
atctggctgt	ttgggcccgc	caccaccggc	aagaccaaca	ttgcggaagc	catcgccac	1380
gccgtgccct	tctacggctg	cgtcaactgg	accaatgaga	actttccctt	caacgattgc	1440
gtcgacaaga	tgggtgatctg	gtgggaggag	ggcaagatga	cggccaaggt	cgtggagtcc	1500
gccaaggcca	ttctcggcgg	cagcaagggtg	cgcggtggacc	aaaagtgcaa	gtcgtccgcc	1560
cagatcgacc	ccacccccgt	gatcgtcacc	tccaacacca	acatgtgcgc	cgtgattgac	1620
gggaacagca	ccaccttcga	gcaccagcag	ccgttgcaag	accggatggt	caaatttgaa	1680
ctcaccgcc	gtctggagca	cgactttggc	aaggtgacga	agcaggaagt	caaagagttc	1740
ttccgctggg	ccagtgatca	cgtgaccgag	gtggcgcatg	agttctacgt	cagaaagggc	1800
ggagccagca	aaagaccgcg	ccccgatgac	gcggatataa	gcgagcccaa	gcgggcctgc	1860
ccctcagtcg	cggatccatc	gacgtcagac	gcggaaggag	ctccggtgga	ctttgccgac	1920
aggtaccaaa	acaaatgttc	tcgtcacgcg	ggcatgattc	agatgctggt	tccctgcaaa	1980
acgtgcgaga	gaatgaatca	gaatttcaac	atttgcttca	cacacggggt	cagagactgt	2040
ttagagtgtt	tcccggcgct	gtcagaatct	caaccggctg	tcagaaaaaa	gacgtatcgg	2100
aaactctgcg	cgattcatca	tctgctgggg	cgggcgccc	agattgcttg	ctcggcctgc	2160
gacctggtca	acgtggacct	ggacgactgc	gtttctgagc	aataaatgac	ttaaaccagg	2220
tatggctgcc	gatggttatc	ttccagattg	gtctcaggac	aacctctctg	agggcattcg	2280
cgagtgggtg	gacctgaaac	ctggagcccc	gaaacccaaa	gccaaccagc	aaaagcagga	2340
caacggccgg	ggtctggtgc	ttcctggcta	caagtacctc	ggacccttca	acggactcga	2400
caagggggag	cccgtcaacg	cggcggacgc	agcggccctc	gagcacgaca	aggcctacga	2460
ccagcagctc	aaagcgggtg	acaatccgta	cctgcggtat	aaccacgccg	acgccgagtt	2520
tcaggagcgt	ctgcaagaag	atacgtcatt	tgggggcaac	ctcgggagag	cagtcttcca	2580
ggccaagaag	cgggttctcg	aacctctcgg	tctggttgag	gaaggcgcta	agacggctcc	2640
tgcaaagaag	agaccggtag	agccgtcacc	tcagcgttcc	cccgaactcct	ccacgggcat	2700
cggcaagaaa	ggccagcagc	ccgccagaaa	gagactcaat	ttcggtcaga	ctggcgactc	2760
agagtgcagc	cccgaacctc	aacctctcgg	agaacctcca	gcagcgccct	ctagtgtggg	2820
atctggtaca	gtggctgcag	gcggtggcgc	accaatggca	gacaataacg	aaggtgccga	2880
cggagtgggt	aatgcctcag	gaaattggca	ttgcgattcc	acatggctgg	gcgacagagt	2940
cattaccacc	agcaccgaa	cctgggccct	gccacctac	aacaaccacc	tctacaagca	3000
aatctccagt	gaaactgcag	gtagtaccaa	cgacaacacc	tacttcggct	acagcacccc	3060

ctgggggtat ttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg 3120  
actcatcaac aacaactggg gattccggcc caagaagctg cggttcaagc tcttcaacat 3180  
ccaggtcaag gaggtcacga cgaatgacgg cgttacgacc atcgctaata accttaccag 3240  
cacgattcag gtattctcgg actcgggaata ccagctgccg tacgtcctcg gctctgcgca 3300  
ccagggtctg ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acggctacct 3360  
gactctcaac aatggcagtc agtctgtggg acgttcctcc ttctactgcc tggagtactt 3420  
ccccctcag atgctgagaa cgggcaacaa ctttgagtgc agctacagct tcgaggacgt 3480  
gcctttccac agcagctacg cacacagcca gagcctggac cggtgatga atccccctcat 3540  
cgaccagtac ttgtactacc tggccagaac acagagtaac ccaggaggca cagctggcaa 3600  
tcggggaactg cagttttacc agggcgggccc ttcaactatg gccgaacaag ccaagaattg 3660  
gttacctgga ccttgcttcc ggcaacaaa agtctcctca acgctggatc aaaacaacaa 3720  
cagcaacttt gcttggaactg gtgccaccaa atatcacctg aacggcagaa actcgttggg 3780  
taatccggcg gtcgccatgg caactcaca ggacgacgag gaccgctttt tcccatccag 3840  
cggagtcctg atttttggaa aaactggagc aactaacaaa actacattgg aaaatgtgtt 3900  
aatgacaaat gaagaagaaa ttcgtcctac taatcctgta gccacggaag aatacgggat 3960  
agtcagcagc aacttacaag cggctaatac tgcagcccag acacaagttg tcaacaacca 4020  
gggagcctta cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtccccatctg 4080  
ggccaagatt cctcacacgg atggcaactt tcacccgtct cttttgatgg gcggctttgg 4140  
acttaaacat ccgcctcctc agatcctgat caagaacact cccgttcccg ctaatcctcc 4200  
ggagggtgtt actcctgcca agtttgcttc gttcatcaca cagtacagca ccggacaagt 4260  
cagcgtggaa atcagatggg agctgcagaa ggaaaacagc aagcgtgga acccggagat 4320  
tcagtacacc tccaactttg aaaagcagac tgggtgtggac ttgtccgttg acagccaggg 4380  
tgtttactct gagcctcgcc ctattggcac tcgttacctc acccgtaatc tgtaattgca 4440  
tgттаатcaa taaaccggtt gattcgtttc agttgaactt tggctctcctg tgcttcttat 4500  
cttatcggtt tccatagcaa ctggttacac attaaactgct tgggtgcgct tcacgataag 4560  
aacactgacg tcaccgcggt acccctagtg atggagtggg ccactccctc tatgcgcgct 4620  
cgctcgtctg gtggggcctg cggaccaaa aggtccgcagac ggagagctc tgctctgccg 4680  
gccccaccga gcgagcgagc gcgcatagag ggagtggcca a 4721

<210> 181  
<211> 737  
<212> PRT  
<213> Unknown

<220>  
<223> capsid protein of adeno-associated virus serotype 7

<400> 181

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
180 185 190  
Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
210 215 220  
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn  
260 265 270  
Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
275 280 285  
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
290 295 300  
Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile  
305 310 315 320  
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
325 330 335  
Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
340 345 350  
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
355 360 365  
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
370 375 380  
Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 182  
<211> 4393  
<212> DNA  
<213> Unknown

<220>  
<223> adeno-associated virus serotype 8

<400> 182  
cagagagggg gtggccaact ccatcactag gggtagcgcg aagcgctcc cagctgccc 60  
cgtcagcgct gacgtaaatt acgtcatagg ggagtggccc tgtattagct gtcacgtgag 120  
tgcttttgcg gcattttgcg acaccacgtg gccatttgag gtatatatgg ccgagtgagc 180  
gagcaggatc tccattttga ccgcgaaatt tgaacgagca gcagccatgc cgggcttcta 240  
cgagatcggt atcaaggtgc cgagcgacct ggacgagcac ctgccgggca tttctgactc 300  
gtttgtgaac tgggtggccg agaaggaatg ggagctgccc ccggattctg acatggatcg 360  
gaatctgatc gagcaggcac ccctgaccgt ggccgagaag ctgcagcgcg acttcctggt 420  
ccaatggcgc cgctgagta agggcccgga ggccctcttc tttgttcagt tcgagaaggg 480  
cgagagctac tttcacctgc acgttctggt cgagaccacg ggggtcaagt ccatggtgct 540  
aggccgcttc ctgagtcaga ttcgggaaaa gcttggcca gaccatctac ccgcggggtc 600  
gagccccacc ttgcccaact ggttcgcggt gaccaaagac gcggtaatgg cgccggcggg 660  
ggggaacaag gtgtgggacg agtgctacat ccccaactac ctctgccc agactcagcc 720  
cgagctgcag tgggcgtgga ctaacatgga ggagtatata agcgcgtgct tgaacctggc 780  
cgagcgcaaa cggctcgtgg cgagcacct gaccacgctc agccagacgc aggagcagaa 840  
caaggagaat ctgaaccca attctgacgc gcccgatgc aggtcaaaaa cctccgcgcg 900  
ctatatggag ctggtcgggt ggctggtgga ccggggcatc acctccgaga agcagtggtg 960  
ccaggaggac caggctcgt acatctcctt caacgccgccc tccaactcgc ggtcccagat 1020  
caaggccgcg ctggacaatg ccggcaagat catggcgctg accaaatccg cgcccgacta 1080  
cctggtgggg ccctcgtgc ccgcggacat taccagaac cgcactacc gcatcctcgc 1140  
tctcaacggc tacgaccctg cctacgccgg ctccgtcttt ctccgctggg ctcaaaaaa 1200  
gttcgggaaa cgcaacacca tctggtgtt tggaccgcc accaccggca agaccaacat 1260  
tgccgaagcc atcgccacg ccgtgccctt ctacggctgc gtcaactgga ccaatgagaa 1320  
ctttcccttc aatgattgcg tcgacaagat ggtgatctgg tgggaggagg gcaagatgac 1380  
ggccaaggtc gtggagtccg ccaaggccat tctcggcggc agcaagggtc gcgtggacca 1440  
aaagtgaag tcgtccgccc agatcgaccc caccgccgtg atcgtcacct ccaacaccaa 1500  
catgtgcgcc gtgattgacg ggaacagcac caccttcgag caccagcagc ctctccagga 1560  
ccggatgttt aagttcgaac tcaccgccg tctggagcac gactttggca aggtgacaaa 1620  
gcaggaagtc aaagagttct tccgtgggc cagtgatcac gtgaccgagg tggcgcatga 1680  
gttttacgtc agaaagggcg gagccagcaa aagaccgcc ccgatgacg cggataaaaag 1740  
cgagcccaag cgggcctgcc cctcagtcgc ggatccatcg acgtcagacg cggaaggagc 1800  
tccggtggac tttccgaca ggtacaaaa caaatgttct cgtcacgcgg gcatgttca 1860  
gatgctgttt ccctgcaaaa cgtgcgagag aatgaatcag aatttcaaca tttgcttcac 1920  
acacggggtc agagactgct cagagtgttt ccccgcggtg tcagaatctc aaccggtcgt 1980  
cagaaagagg acgtatcgga aactctgtgc gattcatcat ctgctggggc gggctcccga 2040

gattgcttgc	tcggcctg	atctggtcaa	cgtaggacctg	gatgactgtg	tttctgagca	2100
ataaatgact	taaaccaggt	atggctgccg	atggttatct	tccagattgg	ctcaggagaca	2160
acctctctga	gggcattcgc	gagtgggtgg	cgctgaaacc	tggagccccg	aagcccaaag	2220
ccaaccagca	aaagcaggac	gacggccggg	gtctgggtgct	tcctggctac	aagtacctcg	2280
gacccttcaa	cggactcgac	aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	2340
agcacgacaa	ggcctacgac	cagcagctgc	aggcgggtga	caatccgtac	ctgcggtata	2400
accacgccga	cgccgagttt	caggagcgct	tgcaagaaga	tacgtctttt	gggggcaacc	2460
tcgggcgagc	agtcttccag	gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	2520
aaggcgctaa	gacggctcct	ggaaagaaga	gaccggtaga	gccatcacc	cagcgttctc	2580
cagactcctc	tacgggcatc	ggcaagaaag	gccaacagcc	cgccagaaaa	agactcaatt	2640
ttggtcagac	tggcgactca	gagtcagttc	cagacctca	acctctcggg	gaacctccag	2700
cagcgccctc	tgggtgtgga	cctaatacaa	tggtgcagg	cggtggcgca	ccaatggcag	2760
acaataacga	aggcgccgac	ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	2820
catggctggg	cgacagagtc	atcaccacca	gcacccgaac	ctgggccctg	cccacctaca	2880
acaaccacct	ctacaagcaa	atctccaacg	ggacatcggg	aggagccacc	aacgacaaca	2940
cctacttcgg	ctacagcacc	ccctgggggt	attttgactt	taacagattc	cactgccact	3000
tttcaccacg	tgactggcag	cgactcatca	acaacaactg	gggattccgg	ccaagagac	3060
tcagcttcaa	gctcttcaac	atccaggcca	aggaggtcac	gcagaatgaa	ggcaccaaga	3120
ccatcgccaa	taacctcacc	agcaccatcc	agggtgtttac	ggactcggag	taccagctgc	3180
cgtacgttct	cggtcttgcc	caccagggct	gcctgcctcc	gttcccggcg	gacgtgttca	3240
tgattcccca	gtacggctac	ctaactctca	acaacggtag	tcaggccgtg	ggacgctcct	3300
ccttctactg	cctggaatac	tttccttcgc	agatgctgag	aaccggcaac	aacttccagt	3360
ttacttacac	cttcgaggac	gtgcctttcc	acagcagcta	cgccacagc	cagagcttgg	3420
accggctgat	gaatcctctg	attgaccagt	acctgtacta	cttgtctcgg	actcaaacaa	3480
caggaggcac	ggcaaatatc	cagactctgg	gcttcagcca	agggtggcct	aatacaatgg	3540
ccaatcaggc	aaagaactgg	ctgccaggac	cctgttaccg	ccaacaacgc	gtctcaacga	3600
caaccgggca	aaacaacaat	agcaactttg	cctggactgc	tgggacaaa	taccatctga	3660
atggaagaaa	ttcattggct	aatcctggca	tcgctatggc	aacacacaaa	gacgacgagg	3720
agcgtttttt	tcccagtaac	gggatcctga	tttttggcaa	acaaaatgct	gccagagaca	3780
atgcggatta	cagcgaatgc	atgctcacca	gcgaggaaga	aatcaaaacc	actaacctg	3840
tggctacaga	ggaatacggg	atcgtggcag	ataacttgca	gcagcaaaac	acggctcctc	3900
aaattggaac	tgtcaacagc	cagggggcct	taccgggtat	ggtctggcag	aaccgggacg	3960
tgtacctgca	gggtcccatc	tgggccaaga	ttcctcacac	ggacggcaac	ttccaccctg	4020
ctccgctgat	gggcggcttt	ggcctgaaac	atcctccgcc	tcagatcctg	atcaagaaca	4080
cgctgtacc	tgcggtatcct	ccgaccacct	tcaaccagtc	aaagtgaac	tctttcatca	4140
cgcaatacag	caccggacag	gtcagcggtg	aaattgaatg	ggagctgcag	aaggaaaaca	4200
gcaagcgctg	gaaccccgag	atccagtaca	cctccaacta	ctacaaatct	acaagtgtgg	4260
actttgctgt	taatacagaa	ggcgtgtact	ctgaaccccg	ccccattggc	acccgttacc	4320
tcacccgtaa	tctgtaattg	cctgttaatc	aataaaccgg	ttgattcggt	tcagttgaac	4380
tttggctctc	gcg					4393

<210> 183  
<211> 738

<212> PRT  
<213> Unknown

<220>  
<223> capsid protein of adeno-associated virus serotype 7

<400> 183

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
180 185 190  
Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220  
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp  
260 265 270  
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285  
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300

Asn 305 Asn Trp Gly Phe Arg 310 Pro Lys Arg Leu Ser 315 Phe Lys Leu Phe Asn 320  
 Ile Gln Val Lys Glu 325 Val Thr Gln Asn Glu 330 Gly Thr Lys Thr Ile 335 Ala  
 Asn Asn Leu Thr 340 Ser Thr Ile Gln Val 345 Phe Thr Asp Ser Glu 350 Tyr Gln  
 Leu Pro Tyr 355 Val Leu Gly Ser Ala 360 His Gln Gly Cys Leu 365 Pro Pro Phe  
 Pro Ala 370 Asp Val Phe Met Ile 375 Pro Gln Tyr Gly Tyr 380 Leu Thr Leu Asn  
 Asn 385 Gly Ser Gln Ala Val 390 Gly Arg Ser Ser Phe 395 Tyr Cys Leu Glu Tyr 400  
 Phe Pro Ser Gln Met 405 Leu Arg Thr Gly Asn 410 Asn Phe Gln Phe Thr Tyr 415  
 Thr Phe Glu Asp 420 Val Pro Phe His Ser 425 Ser Tyr Ala His Ser 430 Gln Ser  
 Leu Asp Arg 435 Leu Met Asn Pro Leu 440 Ile Asp Gln Tyr Leu 445 Tyr Tyr Leu  
 Ser Arg 450 Thr Gln Thr Thr Gly 455 Gly Thr Ala Asn Thr 460 Gln Thr Leu Gly  
 Phe 465 Ser Gln Gly Gly Pro 470 Asn Thr Met Ala Asn 475 Gln Ala Lys Asn Trp 480  
 Leu Pro Gly Pro Cys 485 Tyr Arg Gln Gln Arg 490 Val Ser Thr Thr Thr 495 Gly  
 Gln Asn Asn Asn 500 Ser Asn Phe Ala Trp 505 Thr Ala Gly Thr Lys 510 Tyr His  
 Leu Asn Gly 515 Arg Asn Ser Leu Ala 520 Asn Pro Gly Ile Ala 525 Met Ala Thr  
 His Lys 530 Asp Asp Glu Glu Arg 535 Phe Phe Pro Ser Asn 540 Gly Ile Leu Ile  
 Phe 545 Gly Lys Gln Asn Ala 550 Ala Arg Asp Asn 555 Asp Tyr Ser Asp Val 560  
 Met Leu Thr Ser Glu 565 Glu Glu Ile Lys Thr 570 Thr Asn Pro Val Ala Thr 575  
 Glu Glu Tyr Gly 580 Ile Val Ala Asp Asn 585 Leu Gln Gln Gln Asn 590 Thr Ala  
 Pro Gln Ile 595 Gly Thr Val Asn Ser 600 Gln Gly Ala Leu Pro 605 Gly Met Val  
 Trp Gln 610 Asn Arg Asp Val Tyr 615 Leu Gln Gly Pro Ile 620 Trp Ala Lys Ile  
 Pro 625 His Thr Asp Gly Asn 630 Phe His Pro Ser Pro 635 Leu Met Gly Gly Phe 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 184  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.60

<400> 184

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 185  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.61

<400> 185

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Pro Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Arg Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu

725

730

735

<210> 186  
 <211> 734  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.53

<400> 186

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro  
 180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445  
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala  
 450 455 460  
 Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro  
 465 470 475 480  
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn  
 485 490 495  
 Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg  
 500 505 510  
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp  
 515 520 525  
 Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu  
 530 535 540  
 Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp  
 545 550 555 560  
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly  
 565 570 575  
 Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu  
 580 585 590  
 Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg  
 595 600 605  
 Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp

610                      615                      620  
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His  
 625                      630                      635                      640  
 Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
                     645                      650                      655  
 Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr  
                     660                      665                      670  
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu  
                     675                      680                      685  
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn  
                     690                      695                      700  
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser  
 705                      710                      715                      720  
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                     725                      730

<210> 187  
 <211> 734  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.55

<400> 187

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1                      5                      10                      15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
                     20                      25                      30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
                     35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                     50                      55                      60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
                     85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
                     100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                     115                      120                      125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
                     130                      135                      140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145                      150                      155                      160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
                     165                      170                      175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Cys Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445  
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala  
 450 455 460  
 Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro  
 465 470 475 480  
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn  
 485 490 495  
 Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg  
 Page 315



Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 Page 317

385	390	395	400
Gln Met Leu Arg Thr 405	Gly Asn Asn Phe 410	Gln Phe Ser Tyr Thr 415	Phe Glu
Asp Val Pro Phe His Ser Ser Tyr 420	Ala His Ser Gln Gly 425	Leu Asp Arg	430
Leu Met Asn Pro Leu Ile Asp 435	Gln Tyr Leu Tyr Tyr 440	Leu Asn Arg Thr	445
Gln Thr Ala Ser Gly Thr 450	Gln Gln Ser Arg Leu 455	Leu Phe Ser Gln Ala	460
Gly Pro Thr Ser Met 465	Ser Leu Gln Ala Lys 470	Asn Trp Leu Pro Gly 475	Pro 480
Cys Tyr Arg Gln 485	Gln Arg Leu Ser Lys 490	Gln Ala Asn Asp Asn Asn Asn	495
Ser Asn Phe Pro Trp Thr Gly Ala Thr 500	Lys Tyr His Leu Asn Gly Gly	510	
Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp 515	520	525	
Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu 530	535	540	
Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp 545	550	555	560
Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly 565	570	575	
Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu 580	585	590	
Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg 595	600	605	
Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp 610	615	620	
Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His 625	630	635	640
Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro 645	650	655	
Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr 660	665	670	
Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu 675	680	685	
Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn 690	695	700	
Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser 705	710	715	720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730

<210> 189  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.49

<400> 189

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Lys Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Gly Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu Tyr Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Ser Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
Page 319

275	280	285
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp 290 295 300		
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val 305 310 315 320		
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu 325 330 335		
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr 340 345 350		
Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp 355 360 365		
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser 370 375 380		
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser 385 390 395 400		
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu 405 410 415		
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg 420 425 430		
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr 435 440 445		
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln 450 455 460		
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly 465 470 475 480		
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn 485 490 495		
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly 500 505 510		
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp 515 520 525		
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys 530 535 540		
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr 545 550 555 560		
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr 565 570 575		
Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr 580 585 590		
Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp 595 600 605		

Arg Asp Val His Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 190  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.51

<400> 190

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

165										170										175																																			
Gly	Asp	Ala	Asp	Ser	Val	Pro	Asp	Pro	Gln	Pro	Leu	Gly	Gln	Pro	Pro																																								
			180					185					190																																										
Ala	Ala	Pro	Ser	Gly	Leu	Gly	Thr	Asn	Thr	Met	Ala	Thr	Gly	Ser	Gly																																								
		195					200					205																																											
Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ser																																								
		210			215						220																																												
Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	Ile																																								
		225			230					235					240																																								
Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	Leu																																								
			245						250					255																																									
Tyr	Lys	Gln	Ile	Ser	Ser	Gln	Ser	Gly	Ala	Ser	Asn	Asp	Asn	His	Tyr																																								
		260					265						270																																										
Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His																																								
		275					280					285																																											
Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Asn	Trp																																								
		290				295					300																																												
Gly	Phe	Arg	Pro	Lys	Arg	Leu	Asn	Phe	Lys	Leu	Phe	Asn	Ile	Gln	Val																																								
		305			310					315				320																																									
Lys	Glu	Val	Thr	Gln	Asn	Asp	Gly	Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu																																								
			325						330					335																																									
Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Ser	Glu	Tyr	Gln	Leu	Pro	Tyr																																								
			340					345					350																																										
Val	Leu	Gly	Ser	Ala	His	Gln	Gly	Cys	Leu	Pro	Pro	Phe	Pro	Ala	Asp																																								
		355					360					365																																											
Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Leu	Thr	Leu	Asn	Asn	Gly	Ser																																								
		370				375					380																																												
Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe	Pro	Ser																																								
					390					395					400																																								
Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Thr	Phe	Ser	Tyr	Thr	Phe	Glu																																								
			405						410					415																																									
Asp	Val	Pro	Phe	His	Ser	Gly	Tyr	Ala	His	Ser	Gln	Ser	Leu	Asp	Arg																																								
			420					425					430																																										
Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu	Ser	Thr	Thr																																								
		435				440						445																																											
Asn	Thr	Pro	Ser	Gly	Thr	Thr	Thr	Gln	Ser	Arg	Leu	Gln	Phe	Ser	Gln																																								
		450				455					460																																												
Ala	Gly	Ala	Ser	Asp	Ile	Arg	Asp	Gln	Ser	Arg	Asn	Trp	Leu	Pro	Gly																																								
		465			470					475					480																																								
Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	Lys	Thr	Ser	Ala	Asp	Asn	Asn																																								
				485					490					495																																									

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 191  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.52

<400> 191

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 Page 323

50	55	60
Val Asn Glu Ala Asp 65	Ala Ala Ala Leu Glu 70	His Asp Lys Ala Tyr Asp 75 80
Arg Gln Leu Asp 85	Ser Gly Asp Asn Pro Tyr 90	Leu Lys Tyr Asn His Ala 95
Asp Ala Glu Phe 100	Gln Glu Arg Leu Lys 105	Glu Asp Thr Ser Phe Gly Gly 110
Asn Leu Gly Arg Ala Val 115	Phe Gln Ala Lys Lys Arg 120	Val Leu Glu Pro 125
Leu Gly Leu Val Gly Glu 130	Pro Val Lys Thr Ala 135 140	Pro Gly Lys Lys Arg
Pro Val Glu His Ser 145	Pro Val Glu Pro Asp 150 155	Ser Ser Ser Gly Thr Gly 160
Lys Ala Gly Gln Gln 165	Pro Ala Arg Lys Arg 170	Leu Asn Phe Gly Gln Thr 175
Gly Asp Ala Asp 180	Ser Val Pro Asp Pro 185	Gln Pro Leu Gly Gln Pro Pro 190
Ala Ala Pro Ser Gly 195	Leu Gly Thr Asn Thr Met 200 205	Ala Thr Gly Ser Gly
Ala Pro Met Ala Asp 210	Asn Asn Glu Gly Ala Asp 215 220	Gly Val Gly Asn Ser
Ser Gly Asn Arg His 225	Cys Asp Ser Thr Trp 230 235	Met Gly Asp Arg Val Ile 240
Thr Thr Ser Thr Arg 245	Thr Trp Ala Leu Pro 250	Thr Tyr Asn Asn His Leu 255
Tyr Arg Gln Ile 260	Ser Ser Gln Ser Gly 265	Ala Ser Asn Asp Asn His Tyr 270
Phe Gly Tyr Ser Thr 275	Pro Trp Gly Tyr Phe 280 285	Asp Phe Asn Arg Phe His
Cys His Phe Ser Pro 290	Arg Asp Trp Gln Arg Leu 295 300	Ile Asn Asn Asn Trp
Gly Phe Arg Pro Lys 305	Arg Leu Asn Phe Lys 310 315	Leu Phe Asn Ile Gln Val 320
Lys Glu Val Thr Gln 325	Asn Asp Gly Thr Thr 330	Thr Ile Ala Asn Asn Leu 335
Thr Ser Thr Val 340	Gln Val Phe Thr Asp 345	Ser Glu Tyr Gln Leu Pro Tyr 350
Val Leu Gly Ser Ala 355	His Gln Gly Cys Leu 360 365	Pro Pro Phe Pro Ala Asp
Val Phe Met Val Pro 370	Gln Tyr Gly Tyr Leu 375	Thr Leu Ser Asn Gly Ser 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Pro Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 192  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.56

<400> 192

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ser Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285  
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300  
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320  
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
325 330 335  
Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr  
340 345 350  
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
355 360 365  
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
370 375 380  
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
385 390 395 400  
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
405 410 415  
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
420 425 430  
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
435 440 445  
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
450 455 460  
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
465 470 475 480  
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
485 490 495  
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
500 505 510  
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
515 520 525  
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
530 535 540  
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
545 550 555 560  
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
565 570 575  
Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
580 585 590  
Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 193  
 <211> 734  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.57  
 <400> 193

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Lys  
 20 25 30  
 Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro Gly  
 35 40 45  
 Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val  
 50 55 60  
 Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Arg  
 65 70 75 80  
 Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp  
 85 90 95  
 Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly Asn  
 100 105 110  
 Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu  
 115 120 125  
 Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg Pro  
 130 135 140  
 Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Gly Thr Gly Lys  
 145 150 155 160

Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly  
 165 170 175  
 Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala  
 180 185 190  
 Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly Ala  
 195 200 205  
 Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser  
 210 215 220  
 Gly Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile Thr  
 225 230 235 240  
 Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr  
 245 250 255  
 Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr Phe  
 260 265 270  
 Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys  
 275 280 285  
 His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly  
 290 295 300  
 Phe Arg Pro Lys Arg Leu Asn Leu Lys Leu Phe Asn Ile Gln Val Lys  
 305 310 315 320  
 Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr  
 325 330 335  
 Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr Val  
 340 345 350  
 Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val  
 355 360 365  
 Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln  
 370 375 380  
 Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln  
 385 390 395 400  
 Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp  
 405 410 415  
 Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu  
 420 425 430  
 Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Asn  
 435 440 445  
 Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln Ala  
 450 455 460  
 Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly Pro  
 465 470 475 480  
 Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn Asn  
 485 490 495

Gly Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg  
 500 505 510  
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp  
 515 520 525  
 Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys Gln  
 530 535 540  
 Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr Asp  
 545 550 555 560  
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly  
 565 570 575  
 Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Arg Ala Ala Thr Ser  
 580 585 590  
 Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg  
 595 600 605  
 Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp  
 610 615 620  
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His  
 625 630 635 640  
 Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
 645 650 655  
 Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr  
 660 665 670  
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu  
 675 680 685  
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn  
 690 695 700  
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser  
 705 710 715 720  
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730

<210> 194  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.58

<400> 194

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asp His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Asp Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Arg Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Ile Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ser Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Arg Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 195  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.63

<400> 195

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Pro Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 196  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, clone hu.64

<400> 196

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Leu Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Arg Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 197  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.66

<400> 197

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ala Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Glu Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Cys Ala His Ser Gln Ser  
 420 425 430  
 Ser Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Arg Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 page 339

705                      710                      715                      720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
                               725                                730                                735

Asn Leu

<210> 198  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, clone hu.67

<400> 198

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1                      5                                10                                15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
                               20                                25                                30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Leu  
                               35                                40                                45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                               50                                55                                60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                                70                                75                                80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
                               85                                90                                95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
                               100                                105                                110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                               115                                120                                125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
                               130                                135                                140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145                                150                                155                                160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
                               165                                170                                175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
                               180                                185                                190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
                               195                                200                                205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
                               210                                215                                220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225                                230                                235                                240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
                               245                                250                                255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly

580                      585                      590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
           595                      600                      605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
           610                      615                      620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
           625                      630                      635                      640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
                           645                      650                      655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
                           660                      665                      670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
           675                      680                      685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
           690                      695                      700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
           705                      710                      715                      720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
                           725                      730                      735

Asn Leu

<210> 199  
 <211> 2175  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 5

<400> 199  
 atgtcttttg ttgatcacc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60  
 tttttgggcc ttgaagcggg cccaccgaaa ccaaaacca atcagcagca tcaagatcaa 120  
 gcccggtggtc ttgtgctgcc tgggtataac tatctcggac ccggaacgg tctcgatcga 180  
 ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240  
 cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300  
 gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360  
 aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420  
 ggaaagcggg tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480  
 aagccttcca cctcgtcaga cgccgaagct ggaccagcg gatcccagca gctgcaaadc 540  
 ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgctggagg tggcggccca 600  
 ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660  
 gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720  
 agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780  
 aacgcctact ttggatacag cccccctgg ggggtactttg actttaaccg cttccacagc 840  
 cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccg 900  
 tccctcagag tcaaatctt caacattcaa gtcaagagg tcacgggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag	1020
ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc	1080
tttacgtgc cgcagtacgg ttacgcgacg ctgaaccgag acaacacaga aaatcccacc	1140
gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac	1200
aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt	1260
cagaacctgt tcaagctggc caaccgctg gtggaccagt acttgtaccg cttcgtgagc	1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc	1380
tacaaaaact gggtcccggg gcccatgggc cgaaccagg gctggaacct gggctccggg	1440
gtcaaccgag ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg	1500
agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc	1560
tatgcccctg agaacactat gatcttcaac agccagccgg cgaaccggg caccaccgcc	1620
acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc	1680
gtggcgtaga acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc	1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac	1800
gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc	1860
tctccggcca tgggcggatt cggactcaaa caccaccgc ccatgatgct catcaagaac	1920
acgcctgtgc ccggaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc	1980
cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaactcc	2040
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac	2100
tttgccccg acagaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt	2160
acccgacccc tttaa	2175

<210> 200  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 3-3

<400> 200	
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt	60
gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac	120
aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gaccgggtaa cggactcgac	180
aaaggagagc cggtaacga ggcggacgag gcagccctcg aacacgacaa agcttacgac	240
cagcagctca aggcgggtga caaccctgac ctcaagtaca accacgccga cgccgagttt	300
caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag	360
gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct	420
ggaaagaagg gggctgtaga tcagtctcct caggaaccgg actcatcatc tgggtgtggc	480
aatcggggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag	540
tcagtccag acctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct	600
aatacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaggg tgccgatgga	660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac	720
accaccagca ccagaacctg ggcctgccc acttacaaca accatctcta caagcaaatac	780
tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg	840
tattttgact ttaacagatt cactgccac ttctcaccac gtgactggca gcgactcatt	900

aacaacaact	ggggattccg	gcccaga	aa	ctcagcttca	agctcttcaa	catccaagtt	960
agaggggtca	cgcagaacga	tggcacgacg	actattgcca	ataaccttac	cagcacgggt		1020
caagtgttta	cggactcggg	gtatcagctc	ccgtacgtgc	tcgggtcggc	gcaccaaggc		1080
tgtctccgc	cgtttccagc	ggacgtcttc	atggcccc	agtatggata	cctcaccctg		1140
aacaacggaa	gtcaagcggg	gggacgctca	tccttttact	gcctggagta	cttcccttcg		1200
cagatgctaa	ggactggaaa	taacttccaa	ttcagctata	ccttcgagga	tgtacctttt		1260
cacagcagct	acgctcacag	ccagagtttg	gatcgcttga	tgaatcctct	tattgatcag		1320
tatctgtact	acctgaacag	aacgcaagga	acaacctctg	gaacaaccaa	ccaatcacgg		1380
ctgcttttta	gccaggctgg	gcctcagctc	atgtctttgc	aggccagaaa	ttggctacct		1440
gggccctgct	accggcaaca	gagactttca	aagactgcta	acgacaacaa	caacagtaac		1500
tttcttgga	cagcggccag	caaatatcat	ctcaatggcc	gcgactcgct	ggtgaatcca		1560
ggaccagcta	tggccagtca	caaggacgat	gaagaaaaat	ttttccctat	gcacggcaat		1620
ctaataattg	gcaaagaagg	gacaacggca	agtaacgcag	aattagataa	tgtaatgatt		1680
acggatgaag	aagagattcg	taccaccaat	cctgtggcaa	cagagcagta	tggaactgtg		1740
gcaaataact	tgcagagctc	aaatacagct	cccacgactg	gaactgtcaa	tcatacgggg		1800
gccttacctg	gcatgggtgtg	gcaagatcgt	gacgtgtacc	ttcaaggacc	tatctgggca		1860
aagattcctc	acacggatgg	acactttcat	ccttctcctc	tgatgggagg	ctttggactg		1920
aaacatccgc	ctcctcaa	at	catgatcaaa	aatactccgg	taccggcaaa	tcctccgacg	1980
actttcagcc	cggccaagtt	tgcttcattt	atcactcagt	actccactgg	acaggtcagc		2040
gtggaaattg	agtgggagct	acagaaagaa	aacagcaaac	gttggaatcc	agagattcag		2100
tacacttcca	actacaacaa	gtctgttaat	gtggacttta	ctgtagacac	taatggtgtt		2160
tatagtgaac	ctcgccctat	tggaaccgg	tatctcacac	gaaacttgta	a		2211

<210> 201  
 <211> 2205  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 4-4

<400> 201	
atgactgacg	gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60
tggtggggcg	tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120
gctcgggggt	ttgtgcttcc ggggtacaaa tacctcggac ccgggcaacgg actcgacaag 180
ggggaacccg	tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240
cagctcaagg	ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300
cagcggcttc	agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360
aaaaagaggg	ttcttgaacc tcttggctctg gttgagcaag cgggtgagac ggctcctgga 420
aagaagagac	cggttgattga atccccccag cagcccgaact cctccacggg tatcggcaaa 480
aaaggcaagc	agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540
ggacccccctg	agggatcaac ttccggagcc atgtctgatg acagtgatg gcgtgcagca 600
gctggcggag	ctgcagtcga gggcggaaca ggtgccgatg gagtgggtaa tgcctcgggt 660
gattggcatt	gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720
tgggtcttgc	ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780
aacacctaca	acggattctc cccccctgg ggatactttg acttcaaccg cttccactgc 840
cacttctcac	cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgctggg	tcaaaatctt	caacatccag	gtcaaggagg	tcacgacgtc	gaacggcgag	960
acaacggtgg	ctaataacct	taccagcacg	gttcagatct	ttgcggactc	gtcgtacgaa	1020
ctgccgtacg	tgatggatgc	gggtcaagag	ggcagcctgc	ctccttttcc	caacgacgtc	1080
tttatggtgc	cccagtacgg	ctactgtgga	ctggtgaccg	gcaacacttc	gcagcaacag	1140
actgacagaa	atgccttcta	ctgcctggag	tacttttcctt	cgcagatgct	gcggactggc	1200
aacaactttg	aaattacgta	cagttttgag	aagggtgcctt	tccactcgat	gtacgcgcac	1260
agccagagcc	tggaccggct	gatgaacctt	ctcatcgacc	agtacctgtg	gggactgcaa	1320
tcgaccacca	ccggaaccac	cctgaatgcc	gggactgccca	ccaccaactt	taccaagctg	1380
cggcctacca	actttttcaa	ctttaaaaag	aactggctgc	ccgggccttc	aatcaagcag	1440
cagggtcttct	caaagactgc	caatcaaaac	tacaagatcc	ctgccaccgg	gtcagacagt	1500
ctcatcaaat	acgagacgca	cagcactctg	gacggaagat	ggagtgcctt	gacccccgga	1560
cctccaatgg	ccacggctgg	acctgcggac	agcaagttca	gcaacagcca	gctcatcttt	1620
gcggggccta	aacagaacgg	caacacggcc	accgtacccg	ggactctgat	cttcacctct	1680
gaggaggagc	tggcagccac	caacgccacc	gatacggaca	tgtggggcaa	cctacctggc	1740
ggtgaccaga	gcaacagcaa	cctgccgacc	gtggacagac	tgacagcctt	gggagccgtg	1800
cctggaatgg	tctggcaaaa	cagagacatt	tactaccagg	gtcccatttg	ggccaagatt	1860
cctcataccg	atggacactt	tcacccctca	ccgctgattg	gtgggtttgg	gctgaaacac	1920
ccgcctcttc	aaatttttat	caagaacacc	ccggtacctg	cgaatcctgc	aacgaccttc	1980
agctctactc	cggtaaactc	cttcattact	cagtacagca	ctggccagggt	gtcgggtgcag	2040
attgactggg	agatccagaa	ggagcggctc	aaacgctgga	accccgagggt	ccagtttacc	2100
tccaactacg	gacagcaaaa	ctctctgttg	tgggctcccg	atgcggctgg	gaaatacact	2160
gagcctaggg	ctatcggtac	ccgctacctc	accaccacc	tgtaa		2205

<210> 202  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 1

<400>	202					
atggtctgccg	atggttatct	tccagattgg	ctcaggagca	acctctctga	gggcattcgc	60
gagtgggtgg	acttgaaacc	tggagccccg	aagcccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgcgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcgggt	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaac	gtccggtaga	gcagtcgccca	caagagccag	actcctcctc	gggcatcggc	480
aagacaggcc	agcagcccgc	taaaaagaga	ctcaattttg	gtcagactgg	cgactcagag	540
tcagtccccg	atccacaacc	tctcggagaa	cctccagcaa	cccccgctgc	tgtgggacct	600
actacaatgg	cttcaggcgg	tggcgacca	atggcagaca	ataacgaagg	cgccgacgga	660
gtgggtaatg	cctcaggaaa	ttggcattgc	gattccacat	ggctgggcga	cagagtcac	720
accaccagca	cccgacactg	ggccttgccc	acctacaata	accacctcta	caagcaaata	780
tccagtgcct	caacgggggc	cagcaacgac	aaccactact	tcggctacag	cacccctgg	840

gggtattttg atttcaacag attccactgc cactttttcac cacgtgactg gcagcgactc	900
atcaacaaca attgggggatt ccggcccaag agactcaact tcaaactctt caacatccaa	960
gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg	1020
gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag	1080
ggctgcctcc ctccgttccc ggcggacgtg ttcattgattc cgcaatacgg ctacctgacg	1140
ctcaacaatg gcagccaagc cgtgggacgt tcattcctttt actgcctgga atatttcctt	1200
tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct	1260
ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac	1320
caatacctgt attacctgaa cagaactcaa aatcagtcgg gaagtgccca aaacaaggac	1380
ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct	1440
ggacctgttt atcggcgagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat	1500
tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct	1560
ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgc	1620
atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt	1680
acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg	1740
gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga	1800
gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc	1860
aaaattcctc acacagatgg acactttcac ccgtctcttc ttatgggcgg ctttggactc	1920
aagaaccgcg ctctctagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg	1980
gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt	2040
gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag	2100
tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt	2160
tatactgagc ctgcgcccat tggcaccgtg taccttacct gtcccctgta a	2211

<210> 203  
 <211> 2211  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 6

<400> 203	
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtggtggg acttgaaacc tggagcccc aaacccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgct tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaaga gggttctcga accttttggg ctgggttgagg aagggtgctaa gacggctcct	420
ggaaagaaac gtccggtaga gcagtgcga caagagccag actcctctc gggcattggc	480
aagacaggcc agcagccgcg taaaaagaga ctcaattttg gtcagactgg cgactcagag	540
tcagtccccg acccacaacc tctcggagaa cctccagcaa ccccgctgc tgtgggacct	600
actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga	660
gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcac	720
accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc	780
tccagtgcct caacgggggc cagcaacgac aaccactact tcggctacag caccctctgg	840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc	900
atcaacaaca attggggatt ccggccaag agactcaact tcaagctctt caacatccaa	960
gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg	1020
gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag	1080
ggctgcctcc ctccgttccc ggcgacgtg ttcattgattc cgcagtacgg ctacctaacg	1140
ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca	1200
tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct	1260
ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac	1320
cagtacctgt attacctgaa cagaactcag aatcagtcgg gaagtgccca aaacaaggac	1380
ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaa ctggctacct	1440
ggacctgtt accggcagca gcgcgtttct aaaacaaaa cagacaacaa caacagcaac	1500
tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct	1560
ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcgggtgc	1620
atgatttttg gaaaggagag cgccggagct tcaaactctg cattggacaa tgtcatgatc	1680
acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg	1740
gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga	1800
gccttacctg gaatgggtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc	1860
aaaattcctc acacggatgg acactttcac ccgtctctc tcattggcgg ctttgactt	1920
aagcaccgcg ctctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca	1980
gagttttcgg ctacaaagtt tgcttcattc atcaccaggt attccacagg acaagtgagc	2040
gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag	2100
tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt	2160
tatactgagc ctcgccccat tggcaccgt tacctcacc gtcccctgta a	2211

<210> 204  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.63

<400> 204	
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac	180
aaggagagag cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga caaccgtac cccaagtaca accacgccga cgcggagttc	300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac	540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttg tctgggaact	600
aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgagg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caagcagatt	780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt ccaactgccac ttttcgccac gtgactggca aagactcatc	900
aacaacaatt ggggattccg gccccaaaaga ctcaacttca agctctttta cattcaagtc	960
aaggagggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg	1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttccttct	1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc	1260
cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggctt	1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctaggaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc	1560
ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc	1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg catgattaca	1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggt	1800
cttcaggga tgggtggga ggacagagac gtgtacctgc agggggccat ctgggcaaag	1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaa	1920
cacctcccc cgcagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc	1980
ttcagtgcgg caaagtgtgc ttccttcatt acacagtact ccacggggca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac	2100
acttccaact acaacaaatc tgtaatatg gactttactg tggacactaa tgggtgtgat	2160
tcagagcctc gcccattgg caccaggtag ctgactcgta atctgtaa	2208

<210> 205  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.56

<400> 205	
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctggatac aagtacctcg gacccttcaa cggactcgac	180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctcctc gggaaccgga	480
aaagcgggca accagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac	540
tccgtacctg acccccagcc tctcggacag ccaccagcat cccctctggt tctgggaact	600
aatacgtatg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggga cagagtcgtc	720
accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcagatt	780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt cactgcccac ttttcgccac gcgactggca gagactcatc	900
aacaacaact ggggattccg gccc aaaaga ctcaacttca agctgtttaa cattcaagtc	960
aaggaggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacggtt	1020
cagggtgttta ctgacttggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg	1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct	1200
cagatgcttc gcaccggaaa caactttacc ttcagctaca cttttgaaga cgttccttct	1260
cacagcagct acgctcacag tcaaagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag acaaacact ccaagcggaa ccactacgca gtccaggctt	1380
cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatgg ccagccacaa ggacgatgaa gaaaagtgtt ttcctcaaag cgggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagggt catgattaca	1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt	1800
cttcaggga tggctcggca ggacagagac gtgtacctgc aggggcccac ctgggcaaaa	1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa	1920
cacctcctc cacagattct cattaagaat accccggtag ctgcgaatcc ttcgaccacc	1980
ttcagcgcgg caaagtgtgc ttccttcac acacagtatt ccacggggca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac	2100
acttccaact acaacaatc tgttaatgtg gactttactg tggacactaa tgggggtgtat	2160
tcagagcctc gccctattgg caccagatac ctgactcgta atctgtaa	2208

<210> 206  
 <211> 2205  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.57

<400> 206	
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccaaagcccg cagagcggca taaggacgac	120
agcagggggtc ttgtgcttcc tggatacaag tacctcggac cttcaacgg actcgacaag	180
ggagagccgg tcaacgaggc agacgcgcgc gccctcgagc acgacaaggc ctacgaccgg	240
cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgcccagc ggagtttcag	300
gagcgcctta aagaagatac gtcttttggg ggcaacctcg gacgagcagt cttccaggcg	360
aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac ggctccggga	420
aaaaagaggc ccgtagagca ctctctgtg gagccagact cctcctcggg aaccggaaaa	480
gcgggcaacc agcctgcaag aaaaagattg aatttcggtc agactggaga cgcagactcc	540
gtacctgacc cccagcctct cggacagcca ccagcagccc cctctggtct gggaactaat	600
acgatggcta caggcagtg cgcaccaatg gcagacaata acgagggcgc cgacggagtg	660
ggtaattcct cgggagattg gcattgcatg tccacatgga tgggcgacag agtcatcacc	720





gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt	780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagaggta cgcagaatga cggtagcagc acgattgccataaaccttac cagcacggtt	1020
cagggtgtta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg	1140
aacaacggga gtcaggcagt aggacgtctt tcatcttact gcctggagta ctttccttct	1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttccttct	1260
cacagcggct acgctcacag ccagagctct gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt	1380
cagttttctc aggcgggagc gagtgacatt cgggaccagt ctaggaaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatgg caagccacaa ggacaatgaa gaaaagtgtt ttcctcagag cggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca	1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtacgg ttctgtatct	1740
accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcgtt	1800
cttcaggga tggcttgga ggacagagat gtgtacctc aggggcccac ctgggcaaag	1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaa	1920
cacctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc	1980
ttcagtgcg caaagtgtgc ttccttcac acacagtact ccacgggaca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggaaaac agcaaagct ggaatcccga aattcagtac	2100
acttccaact acaacaagtc tgtaatatg gactttactg tggacactaa tggcgtgtat	2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 209  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.49

<400> 209	
atggctgccc atggttatct tccagattgg ctcaaggaca ctctctctga aggaataaga	60
cagtgggtga agctcaaac tggcccacca ccaccaaac ccgcagagcg gcataaggac	120
gacagcgggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac	180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agtacgaca ggcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaacagga	480
aaagcgggcc agcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac	540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggaact	600
aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgagg cgccgacgga	660

gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatc	780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg gcccagaga ctcaacttca agctctttaa cattcaagtc	960
aaggagggtca cgcagaatga cggtagacg acgattgccataaaccttac cagcacgggt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc ccggctcggc gcatcaagga	1080
tgcctcccg cgttcccagc agacgtcttc atgggtgccac agtatggata cctcacctg	1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttccttct	1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgagga tggtccttct	1260
cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt	1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctaggaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatg ccagccacaa ggacgatgaa gaaaagtgtt ttcctcaaag cggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca	1680
gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct	1740
accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac acaaggcgtt	1800
cttcaggga tggctgga ggacagagac gtgcacctgc aggggcctat ctgggcaaag	1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt tggacttaa	1920
cacctcttc cacagattct catcaagaac accccggtac ctgcaaatcc ttcgaccacc	1980
ttcagtgcgg caaagtgtgc ttccttcac acacagtatt ccacaggga ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaacccga gatccagtac	2100
acttccaact acaacaatc tggtaatgtg gactttactg tggacactaa tgggtgttat	2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 210  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.52

<400> 210	
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga	60
cagtgtgtga agctcaaac tggcccacca ccaccaaac ccgcagagcg gcataaggac	120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac	180
aaggagagc cggtaacga ggacagcgc gcggccctcg agcacgcaa agcctacgac	240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag	360
gcgaaaaaga gggttcttga acctctgggc ctggttggg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga	480
aaggcgggcc agcagcctgc aagaaaaa ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg accccagcc tctcggacag ccaccagcag cccctctgg tctgggaact	600

aatac gatgg	ctacaggcag	tggcgacca	atggcagaca	ataacgaggg	cgccgacgga	660
gtgggtaatt	cctcgggaaa	tcggcattgc	gattccacat	ggatgggcca	cagagtcac	720
accaccagca	cccgaacctg	ggccctgccc	acctacaaca	accacctcta	cagacaaaatt	780
tccagccaat	caggagcctc	gaacgacaat	cactactttg	gctacagcac	cccttggggg	840
tattttgact	tcaacagatt	ccactgccac	ttttcaccac	gtgactggca	aagactcatc	900
aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttaa	cattcaagtc	960
aaagaggcca	cgcagaatga	cggtagcgac	acgattgcc	ataaccttac	cagcacgggt	1020
cagggtgtta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgcctcccgc	cgttcccagc	agacgtcttc	atgggtgccac	agtatggata	cctcacccctg	1140
agcaacggga	gtcaggcagt	aggacgtctc	tcattttact	gcccggagta	ctttccttct	1200
cagatgctgc	gtaccggaaa	caactttacc	ttcagctaca	cttttgagga	cgttcctttc	1260
cacagcagct	acgtcacag	ccagagtctg	gaccgtctca	tgaatcctct	catcgaccag	1320
tacctgtatt	acttgagcac	aacaaacact	ccaagtggaa	ccaccacgca	gtcaaggctt	1380
cagttttctc	aggccggagc	gagtgacatt	cgggaccagt	ctaggaactg	gcttcctgga	1440
ccctgttacc	gccagcagcg	agtatcaaag	acatctcgcg	ataacaacaa	cagtgaatac	1500
tcgtggactg	gagctaccaa	gtaccacctc	aatggcagag	actctctggt	gaatccgggc	1560
ccggccatgg	caagccacaa	ggacaatgaa	gaaaagtgtt	ttcctcagag	cggggttctc	1620
atctttggga	agcaaggctc	agagaaaaca	aatgtggaca	ttgaaaagg	catgattaca	1680
gacgaagagg	aaatcaggac	aaccaatccc	gtggctacgg	agcagtatgg	ttctgtatct	1740
accaacctcc	agagaggcaa	cagacaagca	gctaccgcag	atgtcaacac	acaaggcggt	1800
cttcaggcca	tggctcggca	ggacagagat	gtgtaccttc	agggggcccat	ctgggcaaag	1860
attccacaca	cggacggaca	ttttcacccc	tctcccctca	tgggtggatt	cggacctaaa	1920
cacctcctc	cacagattct	catcaagaac	accccggtac	ctgcgaatcc	ttcgaccacc	1980
ttcagtcggg	caaagtgtgc	ttccttcac	acacagtact	ccacgggaca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	aattcagtac	2100
acttccaact	acaacaagtc	tgttaatgtg	gactttactg	tggacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atttgtaa		2208

<210> 211  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 2

<400> 211						
atggctgccc	atggttatct	tccagattgg	ctcaggagca	ctctctctga	aggaataaga	60
cagtggtgga	agctcaaacc	tggcccacca	ccaccaaac	ccgcagagcg	gcataaggac	120
gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gacccttcaa	cggactcgac	180
aaggggagagc	cggtaacga	ggcagacgcc	gcggccctcg	agcacgacaa	agcctacgac	240
cggcagctcg	acagcggaga	caaccggtac	ctcaagtaca	accacgccga	cgcggaagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcgaaaaaga	gggttcttga	acctctgggc	ctgggtgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
aaggcggggc	agcagcctgc	aagaaaaaga	ttgaattttg	gtcagactgg	agacgcagac	540
tcagtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggaact	600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt	780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt cacttgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagaggta cgcagaatga cggtagacg acgattgccataaaccttac cagcacggtt	1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccgc cgttcccagc agacgtcttc atgggtgccac agtatggata cctcacctg	1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttccttct	1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttccttct	1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaaact ccaagtggaa ccaccacgca gtcaaggctt	1380
cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttctgga	1440
ccctgttacc gccagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca	1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcgtt	1800
cttcaggca tggcttgga ggacagagat gtgtacctc aggggcccat ctgggcaaag	1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaa	1920
cacctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc	1980
ttcagtgcgg caaagtgtgc ttccttcac acacagtact ccacgggaca ggtcagcgtg	2040
gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatccga aattcagtac	2100
acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat	2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa	2208

<210> 212  
 <211> 2208  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.64

<400> 212	
atggctgccg atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga	60
cagtgggtgga agctcaaacc tggcccacca ccacaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gaccttcaa cggactcgac	180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac	240
cggcagctcg acggcggaga caaccgtac ctcaagtaca accacgccga cgggaggttc	300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctctt gcggagccag actcctcctc gggaaccgga	480
aaagcgggcc agcagcctgc aagaaggaga ttgaatttcg gtcagactgg agacgcagac	540

tccgtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggaact	600
aatacgatgg	ctacaggcag	tggcgaccca	atggcagaca	ataacgaggg	cgccgacgga	660
gtgggtaatt	cctcgggaaa	ttggcattgc	gattccacat	ggatgggcga	cagagtcac	720
accaccagca	cccgcacctg	ggctctgccc	acctacaaca	accacctcta	caggcagatt	780
tccagccaat	caggagcctc	aaacgacaac	cactactttg	gctacagcac	cccttggggg	840
tattttgact	tcaacagatt	ccactgccac	ttttcgccac	gtgactggca	aagactcatc	900
aacaacaatt	ggggatcccc	gccccaaa	ctcaacttca	agctctttaa	cattcaagtc	960
aaggaggcca	cgcagaatga	cggtagcagc	acgattgcca	ataaccttac	cagcacggtt	1020
cagggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgcctcccgc	cggtcccagc	agacgtcttc	atggtgccac	agtatggata	cctcaccctg	1140
aacaacggga	gtcaggcagt	aggacgtctt	tcatctttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtaccggaaa	caactttacc	ttcagctaca	cctttgagga	cgttcctttc	1260
cacagcagct	acgcccacag	ccagagtttg	gaccgtctca	tgaatcctct	cgtcgaccag	1320
tacctgtatt	acttgagcag	aacaaacact	ccaagcggaa	ccaccacgca	gtcaaggctt	1380
cagttttctc	aggccggagc	aagtgcattt	cgggaccagt	ctaggaactg	gcttcctgga	1440
ccctgttacc	gccagcagcg	agtatcaaag	acatctgcgg	ataacaaca	cagtgaatac	1500
tcgtggactg	gagctaccaa	gtaccacctt	aatggaagag	actctctggt	gaatccgggc	1560
ccggccatgg	ccagccacaa	ggacgatgaa	gaaaagtgtt	ttcctcagag	cgggggttctc	1620
atctttggaa	aacaagactc	gggaaaaact	aatgtggaca	ttgaaaaggt	catgattaca	1680
gacgaagagg	aaatcaggac	caccaatccc	gtggctacgg	agcagtatgg	ttctgtatct	1740
accaacctcc	agagcggcaa	cacacaagca	gctacctcag	atgtcaacac	acaaggcggt	1800
cttcaggcca	tgggtgtggc	ggacagagac	gtgtacctgc	agggggcccat	ctgggcaaag	1860
attccacaca	cggacggaca	ttttcacccc	tctccctca	tgggcggatt	cggacttaaa	1920
caccctcccc	cgcagattct	catcaagaac	accccggtac	ctgcgaatcc	ttcgactacc	1980
ttcagtgcgg	caaagtttgc	ttccttcatt	acacagtact	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	gattcagtac	2100
acttccaact	acaacaaatc	tgttaatgtg	gactttactg	tggacactaa	tgggtgttat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 213  
 <211> 2214  
 <212> DNA  
 <213> Unknown

<220>  
 <223> adeno-associated virus serotype 7

<400>	213	
atggctgccc	atggttatct	tccagattgg
gagtgggtgg	acctgaaacc	tggagcccc
aacggccggg	gtctgggtgct	tcctggctac
aagggggagc	ccgtcaacgc	ggcggacgca
cagcagctca	aagcgggtga	caatccgtac
caggagcgtc	tgcaagaaga	tacgtcattt
gccaagaagc	gggttctcga	acctctcggt
gcaaagaaga	gaccggtaga	gccgtcacct
ggcaagaaag	gccagcagcc	cgccagaaag
	agactcaatt	tcggtcagac
	tggcgactca	
		60
		120
		180
		240
		300
		360
		420
		480
		540



ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca	540
gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tgggtgtggga	600
cctaatacaa tggctgcagg cgggtggcgca ccaatggcag acaataacga aggcgcccgc	660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcacccgaac ctggggccctg cccacctaca acaaccacct ctacaagcaa	780
atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960
atccagggtca aggagggtcac gcagaatgaa ggcaccaaga ccatcgcaa taacctcacc	1020
agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc	1080
caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac	1140
ctaactctca acaacggtag tcaggccgtg ggacgctcct ctttctactg cctggaatac	1200
tttcccttcg agatgctgag aaccggcaac aacttccagt ttacttacac cttcaggagc	1260
gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg	1320
attgaccagt acctgtacta cttgtctcgg actcaaaca caggaggcac ggcaaatacg	1380
cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg	1440
ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat	1500
agcaactttg cctggactgc tgggacaaa taccatctga atggaagaaa ttcattggct	1560
aatcttgga tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac	1620
gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc	1680
atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacgg	1740
atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc	1800
cagggggcct taccgggtat ggtctggcag aaccgggacg tgtacctgca ggggtccatc	1860
tgggccaaga ttctcacac ggacggcaac ttccaccgt ctccgctgat gggcggcttt	1920
ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct	1980
ccgaccacct tcaaccagtc aaagtgaac tctttcatca cgcaatacag caccggacag	2040
gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgtg gaaccccgag	2100
atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgtgt taatacagaa	2160
ggcgtgtact ctgaaccccg ccccatgtgc acccgttacc tcaccgtaa tctgtaa	2217

<210> 215  
 <211> 2217  
 <212> DNA  
 <213> Unknown

<220>  
 <223> new AAV serotype, clone hu.67

<400> 215	
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac	120
gacggccggg gtctgggtgt tcttggctac aagtacctcg gacccttcaa cggactcgac	180
aaggggggag ccgtcaatgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct	420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc cgactcctc caggggcac	480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540  
 gagtcatgcc ccgacctca accaatcgga gaaccaccag caggcccctc tggcttgga 600  
 tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgcccag 660  
 ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720  
 atcaccacca gacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780  
 atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840  
 ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900  
 cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960  
 atccagggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020  
 agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080  
 caccagggtc gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140  
 cttacactga acaatggaag tcaagccgta ggccgttcct ctttctactg cctggaatat 1200  
 tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260  
 gtgcctttcc acagcggcta cgacacagc cagagcttgg accgactgat gaatcctctc 1320  
 atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaaac tcaagggtacc 1380  
 cagcaattgt tattttctca agctgggcct gcaaacaatgt cggctcaggc taagaactgg 1440  
 ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500  
 agcaactttg cttggactgg tgccacaaa tatcacctga acggaagaga ctctttggta 1560  
 aatcccgggt tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcgagt 1620  
 ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680  
 atgctaacca gcgaagaaga aattaaacc actaacctg tagccacaga acaatacggc 1740  
 gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800  
 caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggccccatc 1860  
 tgggccaaga ttcttcacac ggacggcaac ttccaccctt caccgctaata gggaggattt 1920  
 ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980  
 ccaacgacgt tcagccaggc gaaattggct tccttcatta cgagtacag caccggacag 2040  
 gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaaccagag 2100  
 attcagtaca cttcaaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160  
 ggaacttatt ctgagcctcg cccattgggt actcgttacc tcaccgtaa tctgtaa 2217

<210> 216  
 <211> 724  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, serotype 5

<400> 216

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly  
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val

50	55	60
Asn Arg Ala Asp Glu Val 65 70	Ala Arg Glu His Asp 75	Ile Ser Tyr Asn Glu 80
Gln Leu Glu Ala Gly Asp Asn Pro Tyr 85	Leu Lys Tyr Asn His Ala Asp 90 95	
Ala Glu Phe Gln Glu Lys Leu Ala Asp 100 105	Asp Thr Ser Phe Gly Gly Asn 110	
Leu Gly Lys Ala Val Phe Gln Ala Lys 115 120	Lys Arg Val Leu Glu Pro Phe 125	
Gly Leu Val Glu Glu Gly Ala Lys Thr 130 135	Ala Pro Thr Gly Lys Arg Ile 140	
Asp Asp His Phe Pro Lys Arg Lys Lys 145 150	Ala Arg Thr Glu Glu Asp Ser 155 160	
Lys Pro Ser Thr Ser Ser Asp Ala Glu 165 170	Ala Gly Pro Ser Gly Ser Gln 175	
Gln Leu Gln Ile Pro Ala Gln Pro Ala 180 185	Ser Ser Leu Gly Ala Asp Thr 190	
Met Ser Ala Gly Gly Gly Gly Pro 195 200	Leu Gly Asp Asn Asn Gln Gly Ala 205	
Asp Gly Val Gly Asn Ala Ser Gly Asp 210 215	Trp His Cys Asp Ser Thr Trp 220	
Met Gly Asp Arg Val Val Thr Lys Ser 225 230	Thr Arg Thr Trp Val Leu Pro 235 240	
Ser Tyr Asn Asn His Gln Tyr Arg Glu 245 250	Ile Lys Ser Gly Ser Val Asp 255	
Gly Ser Asn Ala Asn Ala Tyr Phe Gly 260 265	Tyr Ser Thr Pro Trp Gly Tyr 270	
Phe Asp Phe Asn Arg Phe His Ser His 275 280	Trp Ser Pro Arg Asp Trp Gln 285	
Arg Leu Ile Asn Asn Tyr Trp Gly Phe 290 295	Arg Pro Arg Ser Leu Arg Val 300	
Lys Ile Phe Asn Ile Gln Val Lys Glu 305 310	Val Thr Val Gln Asp Ser Thr 315 320	
Thr Thr Ile Ala Asn Asn Leu Thr Ser 325 330	Thr Val Gln Val Phe Thr Asp 335	
Asp Asp Tyr Gln Leu Pro Tyr Val Val 340 345	Gly Asn Gly Thr Glu Gly Cys 350	
Leu Pro Ala Phe Pro Pro Gln Val Phe 355 360	Thr Leu Pro Gln Tyr Gly Tyr 365	
Ala Thr Leu Asn Arg Asp Asn Thr Glu 370 375	Asn Pro Thr Glu Arg Ser Ser 380	

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn  
 385 390 395 400  
 Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser  
 405 410 415  
 Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp  
 420 425 430  
 Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln  
 435 440 445  
 Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp  
 450 455 460  
 Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly  
 465 470 475 480  
 Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu  
 485 490 495  
 Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr  
 500 505 510  
 Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile  
 515 520 525  
 Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu  
 530 535 540  
 Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg  
 545 550 555 560  
 Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser  
 565 570 575  
 Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro  
 580 585 590  
 Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp  
 595 600 605  
 Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met  
 610 615 620  
 Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn  
 625 630 635 640  
 Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser  
 645 650 655  
 Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu  
 660 665 670  
 Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln  
 675 680 685  
 Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp  
 690 695 700  
 Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu  
 705 710 715 720

Thr Arg Pro Leu

<210> 217  
<211> 736  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, serotype 3-3

<400> 217

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro  
20 25 30  
Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly  
130 135 140  
Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly  
145 150 155 160  
Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175  
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
180 185 190  
Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly  
195 200 205  
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220  
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240  
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255  
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285  
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300  
Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320  
Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
325 330 335  
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
340 345 350  
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
355 360 365  
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
370 375 380  
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
385 390 395 400  
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
405 410 415  
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
420 425 430  
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
435 440 445  
Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser  
450 455 460  
Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro  
465 470 475 480  
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn  
485 490 495  
Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn  
500 505 510  
Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys  
515 520 525  
Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly  
530 535 540  
Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile  
545 550 555 560  
Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln  
565 570 575  
Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr  
580 585 590  
Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln  
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala  
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr  
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val  
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 218  
<211> 734  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, serotype 4-4

<400> 218

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu  
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys  
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly  
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val  
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln  
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp  
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn  
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu  
115 120 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro  
130 135 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys  
145 150 155 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr  
 165 170 175  
 Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser  
 180 185 190  
 Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly  
 195 200 205  
 Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys  
 210 215 220  
 Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr  
 225 230 235 240  
 Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu  
 245 250 255  
 Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr  
 260 265 270  
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln  
 275 280 285  
 Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val  
 290 295 300  
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu  
 305 310 315 320  
 Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp  
 325 330 335  
 Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser  
 340 345 350  
 Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr  
 355 360 365  
 Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn  
 370 375 380  
 Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly  
 385 390 395 400  
 Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser  
 405 410 415  
 Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile  
 420 425 430  
 Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu  
 435 440 445  
 Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn  
 450 455 460  
 Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln  
 465 470 475 480  
 Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr  
 485 490 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly  
 500 505 510  
 Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro  
 515 520 525  
 Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys  
 530 535 540  
 Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser  
 545 550 555 560  
 Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly  
 565 570 575  
 Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp  
 580 585 590  
 Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg  
 595 600 605  
 Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp  
 610 615 620  
 Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His  
 625 630 635 640  
 Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
 645 650 655  
 Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr  
 660 665 670  
 Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu  
 675 680 685  
 Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly  
 690 695 700  
 Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr  
 705 710 715 720  
 Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu  
 725 730

<210> 219  
 <211> 736  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, serotype 1

<400> 219

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160  
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190  
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
 260 265 270  
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350  
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
 355 360 365  
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400  
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser  
 450 455 460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505 510  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
 530 535 540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575  
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590  
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
725 730 735

<210> 220  
<211> 736  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, serotype 6

<400> 220

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350  
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
 355 360 365  
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380  
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400  
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser  
 450 455 460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505 510  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
 530 535 540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575  
 Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590  
 Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720  
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735  
  
 <210> 221  
 <211> 735  
 <212> PRT  
 <213> Unknown  
  
 <220>  
 <223> vp1, serotype 2  
  
 <400> 221  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 222  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, serotype 7

<400> 222

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly

705                      710                      715                      720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
                                  725                                   730                                   735

Leu

<210> 223  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, serotype 8

<400> 223

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1                      5                                   10                                   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro  
                                  20                                   25                                   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
                                  35                                   40                                   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
                                  50                                   55                                   60

Val Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                                   70                                   75                                   80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
                                  85                                   90                                   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
                                  100                                   105                                   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
                                  115                                   120                                   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
                                  130                                   135                                   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145                                   150                                   155                                   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
                                  165                                   170                                   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
                                  180                                   185                                   190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly  
                                  195                                   200                                   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
                                  210                                   215                                   220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225                                   230                                   235                                   240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
                                  245                                   250                                   255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly  
 450 455 460  
 Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile  
 530 535 540  
 Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 Page 377



Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160  
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190  
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
 260 265 270  
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350  
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
 355 360 365  
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380  
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400  
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser  
 Page 379

450                      455                      460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465                      470                      475                      480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
                          485                      490                      495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
                          500                      505                      510  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
                          515                      520                      525  
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
                          530                      535                      540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545                      550                      555                      560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
                          565                      570                      575  
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
                          580                      585                      590  
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
                          595                      600                      605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610                      615                      620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625                      630                      635                      640  
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
                          645                      650                      655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
                          660                      665                      670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
                          675                      680                      685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690                      695                      700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705                      710                      715                      720  
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
                          725                      730                      735

<210> 225  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, modified hu.29

<400> 225

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1                      5                      10                      15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 Page 381



Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 226  
<211> 735  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, modified hu.7

<400> 226

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Pro Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile

225	230	235	240
Thr Thr Ser Thr	Arg 245 Thr Trp Ala Leu	Pro 250 Thr Tyr Asn Asn	His 255 Leu
Tyr Lys Gln	Ile 260 Ser Ser Gln Ser	Gly 265 Ala Ser Asn Asp	Asn 270 His Tyr
Phe Gly Tyr	Ser Thr Pro Trp	Gly 280 Tyr Phe Asp Phe	Asn 285 Arg Phe His
Cys His	Phe Ser Pro Arg	Asp 295 Trp Gln Arg Leu	Ile 300 Asn Asn Asn Trp
Gly 305 Phe Arg Pro Lys	Arg 310 Leu Asn Phe Lys	Leu 315 Phe Asn Ile Gln	Val 320
Lys Glu Val Thr	Gln 325 Asn Asp Gly Thr	Thr 330 Thr Thr Ile Ala	Asn 335 Asn Leu
Thr Ser Thr	Val 340 Gln Val Phe Thr	Asp 345 Ser Glu Tyr Gln	Leu 350 Pro Tyr
Val Leu	Gly 355 Ser Ala His Gln	Gly 360 Cys Leu Pro Pro	Phe 365 Pro Ala Asp
Val Phe	Met Val Pro Gln	Tyr 375 Gly Tyr Leu Thr	Leu 380 Asn Asn Gly Ser
Gln Ala Val Gly Arg	Ser 390 Ser Phe Tyr Cys	Leu 395 Glu Tyr Phe Pro	Ser 400
Gln Met Leu Arg	Thr 405 Gly Asn Asn Phe	Gln 410 Phe Ser Tyr Thr	Phe 415 Glu
Asp Val Pro	Phe 420 His Ser Ser Tyr	Ala 425 His Ser Gln Ser	Leu 430 Asp Arg
Leu Met	Asn 435 Pro Leu Ile Asp	Gln 440 Tyr Leu Tyr Tyr	Leu 445 Asn Lys Thr
Gln Ser	Asn Ser Gly Thr	Leu 455 Gln Gln Ser Arg	Leu 460 Leu Phe Ser Gln
Ala Gly Pro Thr Ser	Met 470 Ser Leu Gln Ala	Lys 475 Asn Trp Leu Pro	Gly 480
Pro Cys Tyr Arg	Gln 485 Gln Arg Leu Ser	Lys 490 Gln Ala Asn Asp	Asn 495 Asn
Asn Ser Asn	Phe 500 Pro Trp Thr Ala	Ala 505 Thr Lys Tyr His	Leu 510 Asn Gly
Arg Asp	Ser 515 Leu Val Asn Pro	Gly 520 Pro Ala Met Ala	Ser 525 His Lys Asp
Asp Glu	Glu Lys Phe Phe	Pro 535 Met His Gly Thr	Leu 540 Ile Phe Gly Lys
Gln Gly Thr Asn Ala	Asn 550 Asp Ala Asp Leu	Asp 555 Asn Val Met Ile	Thr 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 227  
 <211> 728  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, modified cy.5

<400> 227

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

115	120	125
Leu Gly 130	Leu Val Glu Glu Gly 135	Ala Lys Thr Ala Pro Gly 140
Pro 145	Ile Glu Ser Pro Asp 150	Ser Ser Thr Gly Ile Gly 155
	Lys Asn Gly Gln	
Pro Pro Ala Lys 165	Lys Leu Asn Phe Gly 170	Gln Thr Gly Asp Ser 175
Ser Val Pro Asp 180	Pro Gln Pro Leu Gly 185	Glu Pro Pro Ala Ala 190
	Pro Ser	
Gly Leu Gly 195	Ser Gly Thr Met Ala 200	Ala Gly Gly Gly Ala 205
	Pro Met Ala	
Asp Asn 210	Asn Glu Gly Ala Asp 215	Gly Val Gly Asn Ala 220
	Ser Gly Asn Trp	
His 225	Cys Asp Ser Thr Trp 230	Leu Gly Asp Arg Val 235
	Ile Thr Thr Ser Thr 240	
Arg Thr Trp Ala 245	Leu Pro Thr Tyr Asn Asn 250	His Leu Tyr Lys Gln 255
	Ile	
Ser Ser Gln 260	Ser Gly Ala Thr Asn Asp 265	Asn His Phe Phe Gly 270
	Tyr Ser	
Thr Pro Trp 275	Gly Tyr Phe Asp Phe 280	Asn Arg Phe His Cys 285
	His Phe Ser	
Pro Arg 290	Asp Trp Gln Arg Leu 295	Ile Asn Asn Asn Trp 300
	Gly Phe Arg Pro	
Arg 305	Lys Leu Arg Phe Lys 310	Leu Phe Asn Ile Gln 315
	Val Lys Glu Val Thr 320	
Thr Asn Asp Gly 325	Val Thr Thr Ile Ala Asn 330	Asn Leu Thr Ser Thr 335
	Ile	
Gln Val Phe 340	Ser Asp Ser Glu Tyr Gln 345	Leu Pro Tyr Val Leu 350
	Gly Ser	
Ala His 355	Gln Gly Cys Leu Pro Pro 360	Phe Pro Ala Asp Val 365
	Phe Met Ile	
Pro Gln 370	Tyr Gly Tyr Leu Thr 375	Leu Asn Asn Gly Ser 380
	Gln Ser Val Gly	
Arg 385	Ser Ser Phe Tyr Cys 390	Leu Glu Tyr Phe Pro 395
	Ser Gln Met Leu Arg 400	
Thr Gly Asn Asn 405	Phe Glu Phe Ser Tyr Thr 410	Phe Glu Glu Val Pro 415
	Phe	
His Ser Ser Tyr 420	Ala His Ser Gln Ser 425	Leu Asp Arg Leu Met 430
	Asn Pro	
Leu Ile 435	Asp Gln Tyr Leu Tyr Tyr 440	Leu Ala Arg Thr Gln 445
	Ser Thr Thr	

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met  
 450 455 460  
 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln  
 465 470 475 480  
 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp  
 485 490 495  
 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn  
 500 505 510  
 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe  
 515 520 525  
 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys  
 530 535 540  
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr  
 545 550 555 560  
 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu  
 565 570 575  
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly  
 580 585 590  
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly  
 595 600 605  
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser  
 610 615 620  
 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu  
 625 630 635 640  
 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro  
 645 650 655  
 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser  
 660 665 670  
 Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn  
 675 680 685  
 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu  
 690 695 700  
 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly  
 705 710 715 720  
 Thr Arg Tyr Leu Thr Arg Asn Leu  
 725

<210> 228  
 <211> 728  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, modified rh.13

<400> 228

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 Page 387

1	5	10	15
Glu Gly Ile	Arg Glu Trp Trp Asp	Leu Lys Pro Gly Ala	Pro Lys Pro
	20	25	30
Lys Ala Asn	Gln Gln Lys Gln Asp Asp Gly Arg Gly	Leu Val Leu Pro	
	35	40	45
Gly Tyr Lys Tyr	Leu Gly Pro Phe Asn Gly	Leu Asp Lys Gly Glu Pro	
	50	55	60
Val Asn Glu Ala Asp	Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp		
	65	70	75
Lys Gln Leu Glu	Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala		
	85	90	95
Asp Ala Glu Phe	Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly		
	100	105	110
Asn Leu Gly Arg Ala Val	Phe Gln Ala Lys Lys Arg Val Leu Glu Pro		
	115	120	125
Leu Gly Leu Val Glu Glu	Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg		
	130	135	140
Pro Ile Glu Ser Pro	Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln		
	145	150	155
Gln Pro Ala Lys	Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu		
	165	170	175
Ser Val Pro Asp	Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser		
	180	185	190
Gly Leu Gly Ser Gly Thr Met	Ala Ala Gly Gly Gly Ala Pro Met Ala		
	195	200	205
Asp Asn Asn Glu Gly Ala	Asp Gly Val Gly Asn Ala Ser Gly Asn Trp		
	210	215	220
His Cys Asp Ser Thr	Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr		
	225	230	235
Arg Thr Trp Ala	Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile		
	245	250	255
Ser Ser Gln Ser Gly Ala Thr	Asn Asp Asn His Phe Phe Gly Tyr Ser		
	260	265	270
Thr Pro Trp Gly Tyr Phe Asp	Phe Asn Arg Phe His Cys His Phe Ser		
	275	280	285
Pro Arg Asp Trp Gln Arg	Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro		
	290	295	300
Arg Lys Leu Arg Phe	Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr		
	305	310	315
Thr Asn Asp Gly Val	Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile		
	325	330	335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser  
 340 345 350  
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile  
 355 360 365  
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly  
 370 375 380  
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg  
 385 390 395 400  
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe  
 405 410 415  
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro  
 420 425 430  
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr  
 435 440 445  
 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met  
 450 455 460  
 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln  
 465 470 475 480  
 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp  
 485 490 495  
 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn  
 500 505 510  
 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe  
 515 520 525  
 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys  
 530 535 540  
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr  
 545 550 555 560  
 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu  
 565 570 575  
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly  
 580 585 590  
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly  
 595 600 605  
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser  
 610 615 620  
 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu  
 625 630 635 640  
 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro  
 645 650 655  
 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser  
 660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn  
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu  
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly  
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 229  
<211> 729  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, modified rh.37

<400> 229

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln  
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu  
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser  
180 185 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala  
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp  
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr  
 225 230 235 240  
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile  
 245 250 255  
 Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350  
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val  
 370 375 380  
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn  
 420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr  
 435 440 445  
 Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr  
 450 455 460  
 Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln  
 465 470 475 480  
 Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala  
 485 490 495  
 Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr  
 500 505 510  
 Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe  
 515 520 525  
 Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn  
 530 535 540  
 Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys  
 545 550 555 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn  
 565 570 575  
 Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln  
 580 585 590  
 Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln  
 595 600 605  
 Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro  
 610 615 620  
 Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile  
 625 630 635 640  
 Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr  
 645 650 655  
 Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val  
 660 665 670  
 Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp  
 675 680 685  
 Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val  
 690 695 700  
 Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile  
 705 710 715 720  
 Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725

<210> 230  
 <211> 737  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, modified rh.67  
 <400> 230

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
450 455 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
465 470 475 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
530 535 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
565 570 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
725 730 735

Leu

<210> 231  
<211> 738  
<212> PRT  
<213> Unknown

<220>

<223> vp1, modified rh.2

<400> 231

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220  
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270  
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285  
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300  
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn  
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala  
 580 585 590  
 Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
660 665 670  
Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
675 680 685  
Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700  
Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720  
Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 232  
<211> 738  
<212> PRT  
<213> Unknown

<220>  
<223> vp1, modified rh.58

<400> 232

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 233  
 <211> 738  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, modified rh.64

<400> 233

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
405 410 415  
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
420 425 430  
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
435 440 445  
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
450 455 460  
Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
465 470 475 480  
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
485 490 495  
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
500 505 510  
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
515 520 525  
Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
530 535 540  
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
545 550 555 560  
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
565 570 575  
Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
580 585 590  
Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
595 600 605  
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
610 615 620  
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
625 630 635 640  
Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
645 650 655  
Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
660 665 670  
Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
675 680 685  
Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700  
Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720  
Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg

725

730

735

Asn Leu

<210> 234  
 <211> 735  
 <212> PRT  
 <213> Unknown

<220>  
 <223> vp1, modified ch.5

<400> 234

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
 180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr  
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285  
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300  
Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320  
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
325 330 335  
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
340 345 350  
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
355 360 365  
Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
370 375 380  
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
385 390 395 400  
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
405 410 415  
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
420 425 430  
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr  
435 440 445  
Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln  
450 455 460  
Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly  
465 470 475 480  
Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn  
485 490 495  
Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly  
500 505 510  
Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp  
515 520 525  
Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys  
530 535 540  
Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr  
545 550 555 560  
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
565 570 575  
Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr  
580 585 590  
Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp

595                      600                      605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610                      615                      620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625                      630                      635                      640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645                      650                      655  
 Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln  
 660                      665                      670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675                      680                      685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690                      695                      700  
 Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr  
 705                      710                      715                      720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725                      730                      735  
  
 <210> 235  
 <211> 736  
 <212> PRT  
 <213> Unknown  
  
 <220>  
 <223> vp1, modified rh.8  
  
 <400> 235  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1                      5                      10                      15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20                      25                      30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50                      55                      60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115                      120                      125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130                      135                      140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145                      150                      155                      160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val  
 435 440 445  
 Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser  
 450 455 460  
 Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn  
 Page 405



Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn  
 260 265 270  
 His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn

370                      375                      380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385                      390                      395                      400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
                     405                      410                      415  
 Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu  
                     420                      425                      430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn  
                     435                      440                      445  
 Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe  
                     450                      455                      460  
 Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu  
 465                      470                      475                      480  
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp  
                     485                      490                      495  
 Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu  
                     500                      505                      510  
 Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His  
                     515                      520                      525  
 Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe  
                     530                      535                      540  
 Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met  
 545                      550                      555                      560  
 Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu  
                     565                      570                      575  
 Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro  
                     580                      585                      590  
 Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp  
                     595                      600                      605  
 Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610                      615                      620  
 His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625                      630                      635                      640  
 Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
                     645                      650                      655  
 Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile  
                     660                      665                      670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
                     675                      680                      685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser  
 690                      695                      700

Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly  
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro  
725 730 735

Leu